

SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT: Choi et. al.

(ii) TITLE OF INVENTION: Streptococcus pneumoniae Antigens and Vaccines

(iii) NUMBER OF SEQUENCES: 452

(iv) CORRESPONDENCE ADDRESS:

- (A) ADDRESSEE: Human Genome Sciences, Inc.
- (B) STREET: 9410 Key West Avenue
- (C) CITY: Rockville
- (D) STATE: Maryland
- (E) COUNTRY: USA
- (F) ZIP: 20850

(v) COMPUTER READABLE FORM:

- (A) MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
- (B) COMPUTER: HP Vectra 486/33
- (C) OPERATING SYSTEM: MSDOS version 6.2
- (D) SOFTWARE: ASCII Text

(vi) CURRENT APPLICATION DATA:

- (A) APPLICATION NUMBER: Unassigned
- (B) FILING DATE: Herewith
- (C) CLASSIFICATION:

(vii) PRIOR APPLICATION DATA:

- (A) APPLICATION NUMBER: 08/961,083
- (B) FILING DATE: OCT-30-1997

(viii) ATTORNEY/AGENT INFORMATION:

- (A) NAME: Michelle S. Marks
- (B) REGISTRATION NUMBER: 41,971
- (C) REFERENCE/DOCKET NUMBER: PB340P2C1

(vi) TELECOMMUNICATION INFORMATION:

- (A) TELEPHONE: (301) 309-8504
- (B) TELEFAX: (301) 309-8512

(2) INFORMATION FOR SEQ ID NO: 1:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1999 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double

(D) TOPOLOGY: linear

----(xi)-SEQUENCE DESCRIPTION: SEQ ID NO: 1:

TAAAATCTAC GACAATAAAA ATCAACTCAT TGCTGACTTG GGTTCCTGAAC GCCGCGTCAA	60
TGCCCCAAGCT AATGATATTC CCACAGATTT GGTTAAGGCA ATCGTTTCTA TCGAAGACCA	120
TCGCTTCTTC GACCACAGGG GGATTGATAC CATCCGTATC CTGGGAGCTT TCTTGCGCAA	180
TCTGCAAAGC AATTCCCTCC AAGGTGGATC AACTCTCACC CAACAGTTGA TTAAGTTGAC	240
TTACTTTTCA ACTTCGACTT CCGACCAGAC TATTTCTCGT AAGGCTCAGG AAGCTTGGTT	300
AGCGATTTCAG TTAGAACAAA AAGCAACCAA GCAAGAAATC TTGACCTACT ATATAAATAA	360
GGTCTACATG TCTAATGGGA ACTATGGAAT GCAGACAGCA GCTCAAAACT ACTATGGTAA	420
AGACCTCAAT AATTTAAGTT TACCTCAGTT AGCCTTGCTG GCTGGAATGC CTCAGGCACC	480
AAACCAATAT GACCCCTATT CACATCCAGA AGCAGCCCAA GACCGCCGAA ACTTGGTCTT	540
ATCTGAAATG AAAAATCAAG GCTACATCTC TGCTGAACAG TATGAGAAAG CAGTCAATAC	600
ACCAATTACT GATGGACTAC AAAGTCTCAA ATCAGCAAGT AATTACCCTG CTTACATGGA	660
TAATTACCTC AAGGAAGTCA TCAATCAAGT TGAAGAAGAA ACAGGCTATA ACCTACTCAC	720
AACTGGGATG GATGTCTACA CAAATGTAGA CCAAGAAGCT CAAAAACATC TGTGGGATAT	780
TTACAATACA GACGAATACG TTGCCTATCC AGACGATGAA TTGCAAGTCG CTTCTACCAT	840
TGTTGATGTT TCTAACGGTA AAGTCATTGC CCAGCTAGGA GCACGCCATC AGTCAAGTAA	900
TGTTTCCTTC GGAATTAACC AAGCAGTAGA AACAAACCGC GACTGGGGAT CAACTATGAA	960
ACCGATCACA GACTATGCTC CTGCCTTGGA GTACGGTGTC TACGATTCAA CTGCTACTAT	1020
CGTTCACGAT GAGCCCTATA ACTACCCTGG GACAAATACT CCTGTTTATA ACTGGGATAG	1080
GGGCTACTTT GGCAACATCA CCTTGCAATA CGCCCTGCAA CAATCGCGAA ACGTCCCAGC	1140
CGTGGAAACT CTAAACAAGG TCGGACTCAA CCGCGCCAAG ACTTTCCTAA ATGGTCTAGG	1200
AATCGACTAC CCAAGTATTC ACTACTCAA TGCCATTTC AAGTAACACAA CCGAATCAGA	1260
CAAAAAATAT GGAGCAAGTA GTGAAAAGAT GGCTGCTGCT TACGCTGCCT TTGCAAAATGG	1320
TGGAACCTAC TATAAACCAA TGTATATCCA TAAAGTCGTC TTTAGTGATG GGAGTGAAAA	1380
AGAGTTCTCT AATGTCGGAA CTCGTGCCAT GAAGGAAACG ACAGCCTATA TGATGACCGA	1440
CATGATGAAA ACAGTCTTGA CTTATGGAAC TGGACGAAAT GCCTATCTTG CTTGGCTCCC	1500
TCAGGCTGGT AAAACAGGAA CCTCTAACTA TACAGACGAG GAAATTGAAA ACCACATCAA	1560
GACCTCTCAA TTTGTAGCAC CTGATGAACT ATTTGCTGGC TATACGCGTA AATATTCAAT	1620
GGCTGTATGG ACAGGCTATT CTAACCGTCT GACACCACTT GTAGGCAATG GCCTTACGGT	1680
CGCTGCCAAA GTTTACCGCT CTATGATGAC CTACCTGTCT GAAGGAAGCA ATCCAGAAGA	1740

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TTGGAATATA CCAGAGGGGC TCTACAGAAA TGGAGAATTC GTATTTAAAA ATGGTGCTCG 1800
 TTCTACGTGG AACTCACCTG CTCCACAACA ACCCCCATCA ACTGAAAGTT CAAGCTCATC 1860
 ATCAGATAGT TCAACTTCAC AGTCTAGCTC AACCACCTCCA AGCACAAATA ATAGTACGAC 1920
 TACCAATCCT AACAATAATA CGCAACAATC AAATACAACC CCTGATCAAC AAAATCAGAA 1980
 TCCTCAACCA GCACAACCA 1999

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 666 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Lys Ile Tyr Asp Asn Lys Asn Gln Leu Ile Ala Asp Leu Gly Ser Glu
 1 5 10 15
 Arg Arg Val Asn Ala Gln Ala Asn Asp Ile Pro Thr Asp Leu Val Lys
 20 25 30
 Ala Ile Val Ser Ile Glu Asp His Arg Phe Phe Asp His Arg Gly Ile
 35 40 45
 Asp Thr Ile Arg Ile Leu Gly Ala Phe Leu Arg Asn Leu Gln Ser Asn
 50 55 60
 Ser Leu Gln Gly Gly Ser Thr Leu Thr Gln Gln Leu Ile Lys Leu Thr
 65 70 75 80
 Tyr Phe Ser Thr Ser Thr Ser Asp Gln Thr Ile Ser Arg Lys Ala Gln
 85 90 95
 Glu Ala Trp Leu Ala Ile Gln Leu Glu Gln Lys Ala Thr Lys Gln Glu
 100 105 110
 Ile Leu Thr Tyr Tyr Ile Asn Lys Val Tyr Met Ser Asn Gly Asn Tyr
 115 120 125
 Gly Met Gln Thr Ala Ala Gln Asn Tyr Tyr Gly Lys Asp Leu Asn Asn
 130 135 140
 Leu Ser Leu Pro Gln Leu Ala Leu Leu Ala Gly Met Pro Gln Ala Pro
 145 150 155 160
 Asn Gln Tyr Asp Pro Tyr Ser His Pro Glu Ala Ala Gln Asp Arg Arg
 165 170 175
 Asn Leu Val Leu Ser Glu Met Lys Asn Gln Gly Tyr Ile Ser Ala Glu
 180 185 190
 Gln Tyr Glu Lys Ala Val Asn Thr Pro Ile Thr Asp Gly Leu Gln Ser
 195 200 205
 Leu Lys Ser Ala Ser Asn Tyr Pro Ala Tyr Met Asp Asn Tyr Leu Lys

210						215						220									
Glu Val Ile Asn Gln Val Glu Glu Glu Thr Gly Tyr Asn Leu Leu Thr 225							230							235							240
Thr Gly Met Asp Val Tyr Thr Asn Val Asp Gln Glu Ala Gln Lys His 245							250							255							
Leu Trp Asp Ile Tyr Asn Thr Asp Glu Tyr Val Ala Tyr Pro Asp Asp 260							265							270							
Glu Leu Gln Val Ala Ser Thr Ile Val Asp Val Ser Asn Gly Lys Val 275							280							285							
Ile Ala Gln Leu Gly Ala Arg His Gln Ser Ser Asn Val Ser Phe Gly 290							295							300							
Ile Asn Gln Ala Val Glu Thr Asn Arg Asp Trp Gly Ser Thr Met Lys 305							310							315							320
Pro Ile Thr Asp Tyr Ala Pro Ala Leu Glu Tyr Gly Val Tyr Asp Ser 325							330							335							
Thr Ala Thr Ile Val His Asp Glu Pro Tyr Asn Tyr Pro Gly Thr Asn 340							345							350							
Thr Pro Val Tyr Asn Trp Asp Arg Gly Tyr Phe Gly Asn Ile Thr Leu 355							360							365							
Gln Tyr Ala Leu Gln Gln Ser Arg Asn Val Pro Ala Val Glu Thr Leu 370							375							380							
Asn Lys Val Gly Leu Asn Arg Ala Lys Thr Phe Leu Asn Gly Leu Gly 385							390							395							400
Ile Asp Tyr Pro Ser Ile His Tyr Ser Asn Ala Ile Ser Ser Asn Thr 405							410							415							
Thr Glu Ser Asp Lys Lys Tyr Gly Ala Ser Ser Glu Lys Met Ala Ala 420							425							430							
Ala Tyr Ala Ala Phe Ala Asn Gly Gly Thr Tyr Tyr Lys Pro Met Tyr 435							440							445							
Ile His Lys Val Val Phe Ser Asp Gly Ser Glu Lys Glu Phe Ser Asn 450							455							460							
Val Gly Thr Arg Ala Met Lys Glu Thr Thr Ala Tyr Met Met Thr Asp 465							470							475							480
Met Met Lys Thr Val Leu Thr Tyr Gly Thr Gly Arg Asn Ala Tyr Leu 485							490							495							
Ala Trp Leu Pro Gln Ala Gly Lys Thr Gly Thr Ser Asn Tyr Thr Asp 500							505							510							
Glu Glu Ile Glu Asn His Ile Lys Thr Ser Gln Phe Val Ala Pro Asp 515							520							525							
Glu Leu Phe Ala Gly Tyr Thr Arg Lys Tyr Ser Met Ala Val Trp Thr 530							535							540							
Gly Tyr Ser Asn Arg Leu Thr Pro Leu Val Gly Asn Gly Leu Thr Val																					

(2) INFORMATION FOR SEQ ID NO: 3:

(A) LENGTH: 1714 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

AAATTACAAT	ACGGACTATG	AATTGACCTC	TGGAGAAAAA	TTACCTCTTC	CTAAAGAGAT	60
TTCAGGTTAC	ACTTATATTG	GATATATCAA	AGAGGGAAAA	ACGACTTCTG	AGTCTGAAGT	120
AAGTAATCAA	AAGAGTTCAG	TTGCCACTCC	TACAAAACAA	CAAAAGGTGG	ATTATAATGT	180
TACACCGAAT	TTTGTAGACC	ATCCATCAAC	AGTACAAGCT	ATTCAGGAAC	AAACACCTGT	240
TTCTTCAACT	AAGCCGACAG	AAGTTCAAGT	AGTTGAAAAA	CCTTTCTCTA	CTGAATTAAT	300
CAATCCAAGA	AAAGAAGAGA	AACAATCTTC	AGATTCTCAA	GAACAATTAG	CCGAACATAA	360
GAATCTAGAA	ACGAAGAAAG	AGGAGAAGAT	TTCTCCAAAA	GAAAAGACTG	GGGTAAATAC	420
ATTAAATCCA	CAGGATGAAG	TTTTATCAGG	TCAATTGAAC	AAACCTGAAC	TCTTATATCG	480
TGAGGAAACT	ATGGAGACAA	AAATAGATTT	TCAAGAAGAA	ATTCAAGAAA	ATCCTGATTT	540
AGCTGAAGGA	ACTGTAAGAG	TAAACAAGA	AGGTAAATTA	GGTAAGAAAG	TTGAAATCGT	600
CAGAATATTC	TCTGTAAACA	AGGAAGAAGT	TTCGCGAGAA	ATTGTTTCAA	CTTCAACGAC	660
TGCGCCTAGT	CCAAGAATAG	TCGAAAAAGG	TACTAAAAAA	ACTCAAGTTA	TAAAGGAACA	720
ACCTGAGACT	GGTGTAGAAC	ATAAGGACGT	ACAGTCTGGA	GCTATTGTTG	AACCCGCAAT	780
TCAGCCTGAG	TTGCCCGAAG	CTGTAGTAAG	TGACAAAAGGC	GAACCAGAAG	TTCAACCTAC	840

ATTACCCGAA GCAGTTGTGA CCGACAAAGG TGAGACTGAG GTTCAACCAG AGTCGCCAGA 900
TACTGTGGTA AGTGATAAAG GTGAACCAGA GCAGGTAGCA CCGCTTCCAG AATATAAGGG 960
TAATATTGAG CAAGTAAAC CTGAAACTCC GGTGAGAAG ACCAAAGAAC AAGGTCCAGA 1020
AAAAACTGAA GAAGTTCAG TAAAACCAAC AGAAGAAACA CCAGTAAATC CAAATGAAGG 1080
TACTACAGAA GGAACCTCAA TTCAAGAAGC AGAAAATCCA GTTCAACCTG CAGAAGAATC 1140
AACAACGAAT TCAGAGAAAG TATCACCAGA TACATCTAGC AAAAATACTG GGAAGTGTC 1200
CAGTAATCCT AGTGATTGCA CAACCTCAGT TGGAGAATCA AATAAACCAG AACATAATGA 1260
CTCTAAAAAT GAAAATTCAG AAAAACTGT AGAAGAAGTT CCAGTAAATC CAAATGAAGG 1320
CACAGTAGAA GGTACCTCAA ATCAAGAAAC AGAAAAACCA GTTCAACCTG CAGAAGAAAC 1380
ACAAACAAAC TCTGGGAAAA TAGCTAACGA AAATACTGGA GAAGTATCCA ATAAACCTAG 1440
TGATTCAAAA CCACCAGTTG AAGAATCAAA TCAACCAGAA AAAAACGGAA CTGCAACAAA 1500
ACCAGAAAAT TCAGGTAATA CAACATCAGA GAATGGACAA ACAGAACCAG AACCATCAAA 1560
CGGAAATTCA ACTGAGGATG TTTCAACCGA ATCAAACACA TCCAATTCAA ATGGAAACGA 1620
AGAAATTAAA CAAGAAAATG AACTAGACCC TGATAAAAAG GTAGAAGAAC CAGAGAAAAC 1680
ACTTGAATTA AGAAATGTTT CCGACCTAGA GTTA 1714

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 571 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Asn Tyr Asn Thr Asp Tyr Glu Leu Thr Ser Gly Glu Lys Leu Pro Leu
1 5 10 15
Pro Lys Glu Ile Ser Gly Tyr Thr Tyr Ile Gly Tyr Ile Lys Glu Gly
20 25 30
Lys Thr Thr Ser Glu Ser Glu Val Ser Asn Gln Lys Ser Ser Val Ala
35 40 45
Thr Pro Thr Lys Gln Gln Lys Val Asp Tyr Asn Val Thr Pro Asn Phe
50 55 60
Val Asp His Pro Ser Thr Val Gln Ala Ile Gln Glu Gln Thr Pro Val
65 70 75 80
Ser Ser Thr Lys Pro Thr Glu Val Gln Val Val Glu Lys Pro Phe Ser
85 90 95
Thr Glu Leu Ile Asn Pro Arg Lys Glu Glu Lys Gln Ser Ser Asp Ser
100 105 110

Glu Thr Glu Lys Pro Val Gln Pro Ala Glu Glu Thr Gln Thr Asn Ser
 450 455 460
 Gly Lys Ile Ala Asn Glu Asn Thr Gly Glu Val Ser Asn Lys Pro Ser
 465 470 475 480
 Asp Ser Lys Pro Pro Val Glu Glu Ser Asn Gln Pro Glu Lys Asn Gly
 485 490 495
 Thr Ala Thr Lys Pro Glu Asn Ser Gly Asn Thr Thr Ser Glu Asn Gly
 500 505 510
 Gln Thr Glu Pro Glu Pro Ser Asn Gly Asn Ser Thr Glu Asp Val Ser
 515 520 525
 Thr Glu Ser Asn Thr Ser Asn Ser Asn Gly Asn Glu Glu Ile Lys Gln
 530 535 540
 Glu Asn Glu Leu Asp Pro Asp Lys Lys Val Glu Glu Pro Glu Lys Thr
 545 550 555 560
 Leu Glu Leu Arg Asn Val Ser Asp Leu Glu Leu
 565 570

(2) INFORMATION FOR SEQ ID NO: 5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 748 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:

TGAGAATCAA GCTACACCCA AAGAGACTAG CGCTCAAAAG ACAATCGTCC TTGCTACAGC	60
TGGCGACGTG CCACCATTG ACTACGAAGA CAAGGGCAAT CTGACAGGCT TTGATATCGA	120
AGTTTTAAAG GCAGTAGATG AAAAAGCTCAG CGACTACGAG ATTCAATTCC AAAGAACCGC	180
CTGGGAGAGC ATCTTCCAG GACTTGATTG TGGTCACTAT CAGGCTGCGG CCAATAACTT	240
GAGTTACACA AAAGAGCGTG CTGAAAAATA CCTTTACTCG CTTCCAATTT CCAACAATCC	300
CCTCGTCCTT GTCAGCAACA AGAAAAATCC TTTGACTTCT CTTGACCAGA TCGCTGGTAA	360
AACAACACAA GAGGATACCG GAACTTCTAA CGCTCAATTC ATCAATAACT GGAATCAGAA	420
ACACACTGAT AATCCCGCTA CAATTAATTT TTCTGGTGAG GATATTGGTA AACGAATCCT	480
AGACCTTGCT AACGGAGAGT TTGATTTCTT AGTTTTTGAC AAGGTATCCG TTCAAAAGAT	540
TATCAAGGAC CGTGGTTTAG ACCTCTCAGT CGTTGATTTA CCTTCTGCAG ATAGCCCCAG	600
CAATTATATC ATTTTCTCAA GCGACCAAAA AGAGTTTAAA GAGCAATTTG ATAAAGCGCT	660
CAAAGAACTC TATCAAGACG GAACCCTTGA AAAACTCAGC AATACCTATC TAGGTGGTTC	720
TTACCTCCCA GATCAATCTC AGTTACAA	748

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 249 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

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Glu Asn Gln Ala Thr Pro Lys Glu Thr Ser Ala Gln Lys Thr Ile Val
1           5           10           15
Leu Ala Thr Ala Gly Asp Val Pro Pro Phe Asp Tyr Glu Asp Lys Gly
          20           25           30
Asn Leu Thr Gly Phe Asp Ile Glu Val Leu Lys Ala Val Asp Glu Lys
          35           40           45
Leu Ser Asp Tyr Glu Ile Gln Phe Gln Arg Thr Ala Trp Glu Ser Ile
          50           55           60
Phe Pro Gly Leu Asp Ser Gly His Tyr Gln Ala Ala Ala Asn Asn Leu
          65           70           75           80
Ser Tyr Thr Lys Glu Arg Ala Glu Lys Tyr Leu Tyr Ser Leu Pro Ile
          85           90           95
Ser Asn Asn Pro Leu Val Leu Val Ser Asn Lys Lys Asn Pro Leu Thr
          100          105          110
Ser Leu Asp Gln Ile Ala Gly Lys Thr Thr Gln Glu Asp Thr Gly Thr
          115          120          125
Ser Asn Ala Gln Phe Ile Asn Asn Trp Asn Gln Lys His Thr Asp Asn
          130          135          140
Pro Ala Thr Ile Asn Phe Ser Gly Glu Asp Ile Gly Lys Arg Ile Leu
          145          150          155          160
Asp Leu Ala Asn Gly Glu Phe Asp Phe Leu Val Phe Asp Lys Val Ser
          165          170          175
Val Gln Lys Ile Ile Lys Asp Arg Gly Leu Asp Leu Ser Val Val Asp
          180          185          190
Leu Pro Ser Ala Asp Ser Pro Ser Asn Tyr Ile Ile Phe Ser Ser Asp
          195          200          205
Gln Lys Glu Phe Lys Glu Gln Phe Asp Lys Ala Leu Lys Glu Leu Tyr
          210          215          220
Gln Asp Gly Thr Leu Glu Lys Leu Ser Asn Thr Tyr Leu Gly Gly Ser
          225          230          235          240
Tyr Leu Pro Asp Gln Ser Gln Leu Gln
          245

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(2) INFORMATION FOR SEQ ID NO: 7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 985 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:

TGGTAACCGC TCTTCTCGTA ACGCAGCTTC ATCTTCTGAT GTGAAGACAA AAGCAGCAAT 60
 CGTCACTGAT ACTGGTGGTG TTGATGACAA ATCATTCAAC CAATCAGCTT GGGAAGGTTT 120
 GCAGGCTTGG GGTAAGAAGC ACAATCTTTC AAAAGATAAC GGTTTCACTT ACTTCCAATC 180
 AACAAGTGAA GCTGACTACG CTAACAACCT GCAACAAGCG GCTGGAAGTT ACAACCTAAT 240
 CTTCCGGTGTT GGTTTTGCCC TTAATAATGC AGTTAAAGAT GCAGCAAAAG AACACACTGA 300
 CTTGAACTAT GTCTTGATTG ATGATGTGAT TAAAGACCAA AAGAATGTTG CGAGCGTAAC 360
 TTTCGCTGAT AATGAGTCAG GTTACCTTGC AGGTGTGGCT GCAGCAAAAA CAACTAAGAC 420
 AAAACAAGTT GGTTTTGTAG GTGGTATCGA ATCTGAAGTT ATCTCTCGTT TTGAAGCAGG 480
 ATTCAAGGCT GGTGTTGCGT CAGTAGACCC ATCTATCAAA GTCCAAGTTG ACTACGCTGG 540
 TTCATTTGGT GATGCGGCTA AAGGTAAAAC AATTGCAGCC GCACAATACG CAGCCGGTGC 600
 AGATATTGTT TACCAAGTAG CTGGTGGTAC AGGTGCAGGT GTCTTTGCAG AGGCAAAATC 660
 TCTCAACGAA AGCCGTCCTG AAAATGAAAA AGTTTGGGTT ATCGGTGTTG ATCGTGACCA 720
 AGAAGCAGAA GGTAATACA CTTCTAAAGA TGGCAAAGAA TCAAACCTTG TTCTTGATATC 780
 TACTTTGAAA CAAGTTGGTA CAACTGTAAA AGATATTTCT AACAAGGCAG AAAGAGGAGA 840
 ATTCCCTGGC GGTCAAGTGA TCGTTTACTC ATTGAAGGAT AAAGGGGTTG ACTTGGCAGT 900
 AACAAACCTT TCAGAAGAAG GTAAAAAAGC TGTCGAAGAT GCAAAAGCTA AAATCCTTGA 960
 TGGAAGCGTA AAAGTTCCTG AAAAA 985

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 328 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Gly Asn Arg Ser Ser Arg Asn Ala Ala Ser Ser Ser Asp Val Lys Thr
 1 5 10 15

Lys Ala Ala Ile Val Thr Asp Thr Gly Gly Val Asp Asp Lys Ser Phe
 20 25 30

Asn Gln Ser Ala Trp Glu Gly Leu Gln Ala Trp Gly Lys Glu His Asn

35	40	45
Leu Ser Lys Asp Asn Gly Phe Thr Tyr Phe Gln Ser Thr Ser Glu Ala		
50	55	60
Asp Tyr Ala Asn Asn Leu Gln Gln Ala Ala Gly Ser Tyr Asn Leu Ile		
65	70	75
Phe Gly Val Gly Phe Ala Leu Asn Asn Ala Val Lys Asp Ala Ala Lys		
	85	90
Glu His Thr Asp Leu Asn Tyr Val Leu Ile Asp Asp Val Ile Lys Asp		
	100	105
Gln Lys Asn Val Ala Ser Val Thr Phe Ala Asp Asn Glu Ser Gly Tyr		
	115	120
Leu Ala Gly Val Ala Ala Ala Lys Thr Thr Lys Thr Lys Gln Val Gly		
130	135	140
Phe Val Gly Gly Ile Glu Ser Glu Val Ile Ser Arg Phe Glu Ala Gly		
145	150	155
Phe Lys Ala Gly Val Ala Ser Val Asp Pro Ser Ile Lys Val Gln Val		
	165	170
Asp Tyr Ala Gly Ser Phe Gly Asp Ala Ala Lys Gly Lys Thr Ile Ala		
	180	185
Ala Ala Gln Tyr Ala Ala Gly Ala Asp Ile Val Tyr Gln Val Ala Gly		
	195	200
Gly Thr Gly Ala Gly Val Phe Ala Glu Ala Lys Ser Leu Asn Glu Ser		
210	215	220
Arg Pro Glu Asn Glu Lys Val Trp Val Ile Gly Val Asp Arg Asp Gln		
225	230	235
Glu Ala Glu Gly Lys Tyr Thr Ser Lys Asp Gly Lys Glu Ser Asn Phe		
	245	250
Val Leu Val Ser Thr Leu Lys Gln Val Gly Thr Thr Val Lys Asp Ile		
	260	265
Ser Asn Lys Ala Glu Arg Gly Glu Phe Pro Gly Gly Gln Val Ile Val		
	275	280
Tyr Ser Leu Lys Asp Lys Gly Val Asp Leu Ala Val Thr Asn Leu Ser		
290	295	300
Glu Glu Gly Lys Lys Ala Val Glu Asp Ala Lys Ala Lys Ile Leu Asp		
305	310	315
Gly Ser Val Lys Val Pro Glu Lys		
	325	

(2) INFORMATION FOR SEQ ID NO: 9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1404 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9:

TGTGGAAATT TGACAGGTAA CAGCAAAAAA GCTGCTGATT CAGGTGACAA ACCTGTTATC 60
 AAAATGTACC AAATCGGTGA CAAACCAGAC AACTTGGATG AATTGTTAGC AAATGCCAAC 120
 AAAATCATTG AAGAAAAAGT TGGTGCCAAA TTGGATATCC AATACCTTGG CTGGGGTGAC 180
 TATGGTAAGA AAATGTCAGT TATCACATCA TCTGGTGAAA ACTATGATAT TGCCTTTGCA 240
 GATAACTATA TTGTAAATGC TCAAAAAGGT GCTTACGCTG ACTTGACAGA ATTGTACAAA 300
 AAAGAAGGTA AAGACCTTTA CAAAGCACTT GACCCAGCTT ACATCAAGGG TAATACTGTA 360
 AATGGTAAGA TTTACGCTGT TCCAGTTGCA GCCAACGTTG CATCATCTCA AAACCTTGCC 420
 TTCAACGGAA CTCTCCTTGC TAAATATGGT ATCGATATTT CAGGTGTTAC TTCTTACGAA 480
 ACTCTTGAGC CAGTCTTGAA ACAAATCAAA GAAAAAGCTC CAGACGTAGT ACCATTTGCT 540
 ATTGGTAAAG TTTTCATCCC ATCTGATAAT TTTGACTACC CAGTAGCAAA CGGTCTTCCA 600
 TTCGTTATCG ACCTTGAAGG CGATACTACT AAAGTTGTAA ACCGTTACGA AGTGCCTCGT 660
 TTCAAAGAAC ACTTGAAGAC TCTTCACAAA TTCTATGAAG CTGGCTACAT TCCAAAAGAC 720
 GTCGCAACAA GCGATACTTC CTTTGACCTT CAACAAGATA CTTGGTTCGT TCGTGAAGAA 780
 ACAGTAGGAC CAGCTGACTA CGGTAACAGC TTGCTTTTAC GTGTTGCCAA CAAAGATATC 840
 CAAATCAAAC CAATTACTAA CTTTCATCAAG NAAAACCAAA CAACACAAGT TGCTAACTTT 900
 GTCATCTCAA ACAACTCTAA GAACAAAGAA AAATCAATGG AAATCTTGAA CCTCTTGAAT 960
 ACGAACCCAG AACTCTTGAA CGGTCTTGTT TACGGTCCAG AAGGCAAGAA CTGGGAAAAA 1020
 ATTGAAGGTA AAGAAAACCG TGTTGCGGTT CTTGATGGCT ACAAAGGAAA CACTCACATG 1080
 GGTGGATGGA ACACTGGTAA CAACTGGATC CTTTACATCA ACGAAAACGT TACAGACCAA 1140
 CAAATCGAAA ATTCTAAGAA AGAATTGGCA GAAGCTAAAG AATCTCCAGC GCTTGGATTT 1200
 ATCTTCAATA CTGACAATGT GAAATCTGAA ATCTCAGCTA TTGCTAACAC AATGCAACAA 1260
 TTTGATACAG CTATCAACAC TGGTACTGTA GACCCAGATA AAGCGATTCC AGAATTGATG 1320
 GAAAAATTGA AATCTGAAGG TGCCTACGAA AAAGTATTGA ACGAAATGCA AAAACAATAC 1380
 GATGAATTCT TGAAAAACAA AAAA 1404

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 468 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

Cys	Gly	Asn	Leu	Thr	Gly	Asn	Ser	Lys	Lys	Ala	Ala	Asp	Ser	Gly	Asp	1	5	10	15
Lys	Pro	Val	Ile	Lys	Met	Tyr	Gln	Ile	Gly	Asp	Lys	Pro	Asp	Asn	Leu	20	25	30	
Asp	Glu	Leu	Leu	Ala	Asn	Ala	Asn	Lys	Ile	Ile	Glu	Glu	Lys	Val	Gly	35	40	45	
Ala	Lys	Leu	Asp	Ile	Gln	Tyr	Leu	Gly	Trp	Gly	Asp	Tyr	Gly	Lys	Lys	50	55	60	
Met	Ser	Val	Ile	Thr	Ser	Ser	Gly	Glu	Asn	Tyr	Asp	Ile	Ala	Phe	Ala	65	70	75	80
Asp	Asn	Tyr	Ile	Val	Asn	Ala	Gln	Lys	Gly	Ala	Tyr	Ala	Asp	Leu	Thr	85	90	95	
Glu	Leu	Tyr	Lys	Lys	Glu	Gly	Lys	Asp	Leu	Tyr	Lys	Ala	Leu	Asp	Pro	100	105	110	
Ala	Tyr	Ile	Lys	Gly	Asn	Thr	Val	Asn	Gly	Lys	Ile	Tyr	Ala	Val	Pro	115	120	125	
Val	Ala	Ala	Asn	Val	Ala	Ser	Ser	Gln	Asn	Phe	Ala	Phe	Asn	Gly	Thr	130	135	140	
Leu	Leu	Ala	Lys	Tyr	Gly	Ile	Asp	Ile	Ser	Gly	Val	Thr	Ser	Tyr	Glu	145	150	155	160
Thr	Leu	Glu	Pro	Val	Leu	Lys	Gln	Ile	Lys	Glu	Lys	Ala	Pro	Asp	Val	165	170	175	
Val	Pro	Phe	Ala	Ile	Gly	Lys	Val	Phe	Ile	Pro	Ser	Asp	Asn	Phe	Asp	180	185	190	
Tyr	Pro	Val	Ala	Asn	Gly	Leu	Pro	Phe	Val	Ile	Asp	Leu	Glu	Gly	Asp	195	200	205	
Thr	Thr	Lys	Val	Val	Asn	Arg	Tyr	Glu	Val	Pro	Arg	Phe	Lys	Glu	His	210	215	220	
Leu	Lys	Thr	Leu	His	Lys	Phe	Tyr	Glu	Ala	Gly	Tyr	Ile	Pro	Lys	Asp	225	230	235	240
Val	Ala	Thr	Ser	Asp	Thr	Ser	Phe	Asp	Leu	Gln	Gln	Asp	Thr	Trp	Phe	245	250	255	
Val	Arg	Glu	Glu	Thr	Val	Gly	Pro	Ala	Asp	Tyr	Gly	Asn	Ser	Leu	Leu	260	265	270	
Ser	Arg	Val	Ala	Asn	Lys	Asp	Ile	Gln	Ile	Lys	Pro	Ile	Thr	Asn	Phe	275	280	285	
Ile	Lys	Xaa	Asn	Gln	Thr	Thr	Gln	Val	Ala	Asn	Phe	Val	Ile	Ser	Asn	290	295	300	
Asn	Ser	Lys	Asn	Lys	Glu	Lys	Ser	Met	Glu	Ile	Leu	Asn	Leu	Leu	Asn	305	310	315	320
Thr	Asn	Pro	Glu	Leu	Leu	Asn	Gly	Leu	Val	Tyr	Gly	Pro	Glu	Gly	Lys				

325 330 335
 Asn Trp Glu Lys Ile Glu Gly Lys Glu Asn Arg Val Arg Val Leu Asp
 340 345 350
 Gly Tyr Lys Gly Asn Thr His Met Gly Gly Trp Asn Thr Gly Asn Asn
 355 360 365
 Trp Ile Leu Tyr Ile Asn Glu Asn Val Thr Asp Gln Gln Ile Glu Asn
 370 375 380
 Ser Lys Lys Glu Leu Ala Glu Ala Lys Glu Ser Pro Ala Leu Gly Phe
 385 390 395 400
 Ile Phe Asn Thr Asp Asn Val Lys Ser Glu Ile Ser Ala Ile Ala Asn
 405 410 415
 Thr Met Gln Gln Phe Asp Thr Ala Ile Asn Thr Gly Thr Val Asp Pro
 420 425 430
 Asp Lys Ala Ile Pro Glu Leu Met Glu Lys Leu Lys Ser Glu Gly Ala
 435 440 445
 Tyr Glu Lys Val Leu Asn Glu Met Gln Lys Gln Tyr Asp Glu Phe Leu
 450 455 460
 Lys Asn Lys Lys
 465

(2) INFORMATION FOR SEQ ID NO: 11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 937 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 11:

TGGTCAAGGA ACTGCTTCTA AAGACAACAA AGAGGCAGAA CTTAAGAAGG TTGACTTTAT	60
CCTAGACTGG ACACCAAATA CCAACCACAC AGGGCTTTAT GTTGCCAAGG AAAAAGGTTA	120
TTTCAAAGAA GCTGGAGTGG ATGTTGATTT GAAATTGCCA CCAGAAGAAA GTTCTTCTGA	180
CTTG GTTATC AACGGAAGG CACCATTTC AGTGTATTC CAAGACTACA TGGCTAAGAA	240
ATTGGAAAAA GGAGCAGGAA TCACTGCCGT TGCAGCTATT GTTGAACACA ATACATCAGG	300
AATCATCTCT CGTAAATCTG ATAATGTAAG CAGTCCAAAA GACTTGGTTG GTAAGAAATA	360
TGGGACATGG AATGACCCAA CTGAACTTGC TATGTTGAAA ACCTTGGTAG AATCTCAAGG	420
TGGAGACTTT GAGAAGGTTG AAAAAGTACC AAATAACGAC TCAAAC TCAACCCGAT	480
TGCCAATGGC GTCTTTGATA CTGCTTGGAT TTACTACGGT TGGGATGGTA TCCTTGCTAA	540
ATCTCAAGGT GTAGATGCTA ACTTCATGTA CTTGAAAGAC TATGTCAAGG AGTTTGACTA	600
CTATTCACCA GTTATCATCG CAAACAACGA CTATCTGAAA GATAACAAAG AAGAAGCTCG	660
CAAAGTCATC CAAGCCATCA AAAAAGGCTA CCAATATGCC ATGGAACATC CAGAAGAAGC	720

TGCAGATATT CTCATCAAGA ATGCACCTGA ACTCAAGGAA AAACGTGACT TTGTCATCGA 780
 ATCTCAAAAA TACTTGTCAA AAGAATACGC AAGCGACAAG GAAAAATGGG GTCAATTTGA 840
 CGCAGCTCGC TGAATGCTT TCTACAAATG GGATAAAGAA AATGGTATCC TTAAAGAAGA 900
 CTTGACAGAC AAAGGCTTCA CCAACGAATT TGTGAAA 937

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 312 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

Gly	Gln	Gly	Thr	Ala	Ser	Lys	Asp	Asn	Lys	Glu	Ala	Glu	Leu	Lys	Lys	1	5	10	15
Val	Asp	Phe	Ile	Leu	Asp	Trp	Thr	Pro	Asn	Thr	Asn	His	Thr	Gly	Leu	20	25	30	
Tyr	Val	Ala	Lys	Glu	Lys	Gly	Tyr	Phe	Lys	Glu	Ala	Gly	Val	Asp	Val	35	40	45	
Asp	Leu	Lys	Leu	Pro	Pro	Glu	Glu	Ser	Ser	Ser	Asp	Leu	Val	Ile	Asn	50	55	60	
Gly	Lys	Ala	Pro	Phe	Ala	Val	Tyr	Phe	Gln	Asp	Tyr	Met	Ala	Lys	Lys	65	70	75	80
Leu	Glu	Lys	Gly	Ala	Gly	Ile	Thr	Ala	Val	Ala	Ala	Ile	Val	Glu	His	85	90	95	
Asn	Thr	Ser	Gly	Ile	Ile	Ser	Arg	Lys	Ser	Asp	Asn	Val	Ser	Ser	Pro	100	105	110	
Lys	Asp	Leu	Val	Gly	Lys	Lys	Tyr	Gly	Thr	Trp	Asn	Asp	Pro	Thr	Glu	115	120	125	
Leu	Ala	Met	Leu	Lys	Thr	Leu	Val	Glu	Ser	Gln	Gly	Gly	Asp	Phe	Glu	130	135	140	
Lys	Val	Glu	Lys	Val	Pro	Asn	Asn	Asp	Ser	Asn	Ser	Ile	Thr	Pro	Ile	145	150	155	160
Ala	Asn	Gly	Val	Phe	Asp	Thr	Ala	Trp	Ile	Tyr	Tyr	Gly	Trp	Asp	Gly	165	170	175	
Ile	Leu	Ala	Lys	Ser	Gln	Gly	Val	Asp	Ala	Asn	Phe	Met	Tyr	Leu	Lys	180	185	190	
Asp	Tyr	Val	Lys	Glu	Phe	Asp	Tyr	Tyr	Ser	Pro	Val	Ile	Ile	Ala	Asn	195	200	205	
Asn	Asp	Tyr	Leu	Lys	Asp	Asn	Lys	Glu	Glu	Ala	Arg	Lys	Val	Ile	Gln	210	215	220	

0976271-012204

Ala Ile Lys Lys Gly Tyr Gln Tyr Ala Met Glu His Pro Glu Glu Ala
225 230 235 240

Ala Asp Ile Leu Ile Lys Asn Ala Pro Glu Leu Lys Glu Lys Arg Asp
245 250 255

Phe Val Ile Glu Ser Gln Lys Tyr Leu Ser Lys Glu Tyr Ala Ser Asp
260 265 270

Lys Glu Lys Trp Gly Gln Phe Asp Ala Ala Arg Trp Asn Ala Phe Tyr
275 280 285

Lys Trp Asp Lys Glu Asn Gly Ile Leu Lys Glu Asp Leu Thr Asp Lys
290 295 300

Gly Phe Thr Asn Glu Phe Val Lys
305 310

(2) INFORMATION FOR SEQ ID NO: 13:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 799 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 13:

TAGCTCAGGT GGAAACGCTG GTTCATCCTC TGGAAAAACA ACTGCCAAAG CTCGCACTAT	60
CGATGAAATC AAAAAAGCG GTGAACTGCG AATCGCCGTG TTTGGAGATA AAAAACCGTT	120
TGGCTACGTT GACAATGATG GTTCTACCAA GGTACGCTAC GATATTGAAC TAGGGAACCA	180
ACTAGCTCAA GACCTTGGTG TCAAGGTAA ATACATTTCG GTCGATGCTG CCAACCGTGC	240
GGAATACTTG ATTTCAAACA AGGTAGATAT TACTCTTGCT AACTTTACAG TAACTGACGA	300
ACGTAAGAAA CAAGTTGATT TTGCCCTTCC ATATATGAAA GTTTCTCTGG GTGTGCTATC	360
ACCTAAGACT GGTCTCATT CAGACGTCAA ACAACTTGAA GGTAACCT TAATTGTCAC	420
AAAAGGA 3 ACTGCTGAGA CTTATTTTGA AAAGAATCAT CCAGAAATCA AACTCCAAAA	480
ATACGACCAA TACAGTGACT CTTACCAAGC TCTTCTTGAC GGACGTGGAG ATGCCTTTTC	540
AACTGACAAT ACGGAAGTTC TAGCTTGGGC GCTTGAAAT AAAGGATTTG AAGTAGGAAT	600
TACTTCCCTC GGTGATCCCG ATACCATTGC GGCAGCAGTT CAAAAAGGCA ACCAAGAATT	660
GCTAGACTTC ATCAATAAAG ATATTGAAAA ATTAGGCAAG GAAACTTCT TCCACAAGGC	720
CTATGAAAAG ACACTTCACC CAACCTACGG TGACGCTGCT AAAGCAGATG ACCTGGTTGT	780
TGAAGGTGGA AAAGTTGAT	799

(2) INFORMATION FOR SEQ ID NO:14:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 266 amino acids
 (B) TYPE: amino acid

0095974 042304
1225260

(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

Ser	Ser	Gly	Gly	Asn	Ala	Gly	Ser	Ser	Ser	Gly	Lys	Thr	Thr	Ala	Lys	1	5	10	15
Ala	Arg	Thr	Ile	Asp	Glu	Ile	Lys	Lys	Ser	Gly	Glu	Leu	Arg	Ile	Ala	20	25	30	
Val	Phe	Gly	Asp	Lys	Lys	Pro	Phe	Gly	Tyr	Val	Asp	Asn	Asp	Gly	Ser	35	40	45	
Thr	Lys	Val	Arg	Tyr	Asp	Ile	Glu	Leu	Gly	Asn	Gln	Leu	Ala	Gln	Asp	50	55	60	
Leu	Gly	Val	Lys	Val	Lys	Tyr	Ile	Ser	Val	Asp	Ala	Ala	Asn	Arg	Ala	65	70	75	80
Glu	Tyr	Leu	Ile	Ser	Asn	Lys	Val	Asp	Ile	Thr	Leu	Ala	Asn	Phe	Thr	85	90	95	
Val	Thr	Asp	Glu	Arg	Lys	Lys	Gln	Val	Asp	Phe	Ala	Leu	Pro	Tyr	Met	100	105	110	
Lys	Val	Ser	Leu	Gly	Val	Val	Ser	Pro	Lys	Thr	Gly	Leu	Ile	Thr	Asp	115	120	125	
Val	Lys	Gln	Leu	Glu	Gly	Lys	Thr	Leu	Ile	Val	Thr	Lys	Gly	Thr	Thr	130	135	140	
Ala	Glu	Thr	Tyr	Phe	Glu	Lys	Asn	His	Pro	Glu	Ile	Lys	Leu	Gln	Lys	145	150	155	160
Tyr	Asp	Gln	Tyr	Ser	Asp	Ser	Tyr	Gln	Ala	Leu	Leu	Asp	Gly	Arg	Gly	165	170	175	
Asp	Ala	Phe	Ser	Thr	Asp	Asn	Thr	Glu	Val	Leu	Ala	Trp	Ala	Leu	Glu	180	185	190	
Asn	Lys	Gly	Phe	Glu	Val	Gly	Ile	Thr	Ser	Leu	Gly	Asp	Pro	Asp	Thr	195	200	205	
Ile	Ala	Ala	Ala	Val	Gln	Lys	Gly	Asn	Gln	Glu	Leu	Leu	Asp	Phe	Ile	210	215	220	
Asn	Lys	Asp	Ile	Glu	Lys	Leu	Gly	Lys	Glu	Asn	Phe	Phe	His	Lys	Ala	225	230	235	240
Tyr	Glu	Lys	Thr	Leu	His	Pro	Thr	Tyr	Gly	Asp	Ala	Ala	Lys	Ala	Asp	245	250	255	
Asp	Leu	Val	Val	Glu	Gly	Gly	Lys	Val	Asp	260	265								

(2) INFORMATION FOR SEQ ID NO: 15:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1189 base pairs

(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 15:

CTCCA	ACTAT	GGTAA	ATCTG	CGGAT	GGCAC	AGTGAC	CATC	GAGTAT	TTTCA	ACCAG	AAAAA	60
AGAAAT	GACC	AAAAC	CTTGG	AAGAA	ATCAC	TCGTGA	TTTT	GAGAAG	GAAA	ACCCT	AAGAT	120
CAAGGT	CAAA	GTCGT	CAATG	TACCA	AATGC	TGGTGA	AGTA	TTGAAG	ACAC	GCGTT	CTCGC	180
AGGAGAT	GTG	CCTGAT	GTGG	TCAAT	ATTTA	CCCAC	AGTCC	ATCGAA	CTGC	AAGAAT	GGGC	240
AAAAGC	AGGT	GTTTT	TGAAG	ATTTG	AGCAA	CAAAGA	CTAC	CTGAA	ACGCG	TGAAAA	ATGG	300
CTACGCT	GAA	AAATAT	GCTG	TAAAC	GAAAA	AGTTT	TACAAC	GTTCT	TTTTA	CAGCT	AATGC	360
TTATGGA	AAT	TACTACA	ACA	AAGATA	AAAT	CGAAGA	ACTG	GGCTT	GAAAG	TTCTT	GAAAC	420
CTGGGAT	GAA	TTTGA	ACAGT	TAGTCA	AAGA	TATCGT	TGCT	AAAGG	ACAAA	CACCAT	TTGG	480
AATTGC	AGGT	GCAGAT	GCCT	GGACAC	TCAA	TGGTT	TACAAT	CAATT	AGCCT	TTGCG	ACAGC	540
AACAGGT	GGA	GGAAA	AGAAG	CAAAT	CAATA	CCTTC	GTTAT	TCTCA	ACCAA	ATGCC	ATTAA	600
ATTGTC	GGAT	CCGATT	TATGA	AAGAT	GATAT	CAAGGT	CATG	GACAT	CCTTC	GCATCA	ATGG	660
ATCTA	AGCAA	AAGAAC	TGGG	AAGGT	GCTGG	CTATA	CCGAT	GTTAT	CGGAG	CCTTC	GCACG	720
TGGGGAT	GTG	CTCAT	GACAC	CAAAT	GGGTG	TTGGG	CGATC	ACAGC	GATTA	ATGAAC	AAAAA	780
ACCGAA	CTTT	AAGATT	TGGGA	CCTTC	CATGAT	TCCAGG	AAAAA	GAAAA	AGGAC	AAAGCT	TAAAC	840
CGTTGGT	GCG	GGAGAC	TTGG	CATGGT	CTAT	CTCAGC	CACC	ACCAA	ACATC	CAAAAG	AAGC	900
CAATGC	CCTTT	GTGGA	ATATA	TGACCC	CGTCC	AGAAGT	CATG	CAAAA	ATACT	ACGATG	TGGA	960
CGGATCT	CCA	ACAGC	GATCG	AAGGGG	TCAA	ACAAGC	AGGA	GAAGAT	TCAC	CGCTT	GCTGG	1020
TATGACC	GAA	TATGC	CTTTA	CGGAT	CGTCA	CTTGGT	CTGG	TTGCA	ACAAT	ACTGG	ACCAG	1080
TGAAGC	AGAC	TTCCAT	ACCT	TGACCA	TGAA	CTATGT	CTTG	ACCGGT	GATA	AACAAG	GCGAT	1140
GGTCAAT	GAT	TTGAAT	GCCT	TCTTTA	AACC	GATGAA	AGCG	GATGT	GCGAT			1189

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 396 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

Ser	Asn	Tyr	Gly	Lys	Ser	Ala	Asp	Gly	Thr	Val	Thr	Ile	Glu	Tyr	Phe
1				5				10					15		

Asn Gln Lys Lys Glu Met Thr Lys Thr Leu Glu Glu Ile Thr Arg Asp
 20 25 30
 Phe Glu Lys Glu Asn Pro Lys Ile Lys Val Lys Val Val Asn Val Pro
 35 40 45
 Asn Ala Gly Glu Val Leu Lys Thr Arg Val Leu Ala Gly Asp Val Pro
 50 55 60
 Asp Val Val Asn Ile Tyr Pro Gln Ser Ile Glu Leu Gln Glu Trp Ala
 65 70 75 80
 Lys Ala Gly Val Phe Glu Asp Leu Ser Asn Lys Asp Tyr Leu Lys Arg
 85 90 95
 Val Lys Asn Gly Tyr Ala Glu Lys Tyr Ala Val Asn Glu Lys Val Tyr
 100 105 110
 Asn Val Pro Phe Thr Ala Asn Ala Tyr Gly Ile Tyr Tyr Asn Lys Asp
 115 120 125
 Lys Phe Glu Glu Leu Gly Leu Lys Val Pro Glu Thr Trp Asp Glu Phe
 130 135 140
 Glu Gln Leu Val Lys Asp Ile Val Ala Lys Gly Gln Thr Pro Phe Gly
 145 150 155 160
 Ile Ala Gly Ala Asp Ala Trp Thr Leu Asn Gly Tyr Asn Gln Leu Ala
 165 170 175
 Phe Ala Thr Ala Thr Gly Gly Gly Lys Glu Ala Asn Gln Tyr Leu Arg
 180 185 190
 Tyr Ser Gln Pro Asn Ala Ile Lys Leu Ser Asp Pro Ile Met Lys Asp
 195 200 205
 Asp Ile Lys Val Met Asp Ile Leu Arg Ile Asn Gly Ser Lys Gln Lys
 210 215 220
 Asn Trp Glu Gly Ala Gly Tyr Thr Asp Val Ile Gly Ala Phe Ala Arg
 225 230 235 240
 Gly Asp Val Leu Met Thr Pro Asn Gly Ser Trp Ala Ile Thr Ala Ile
 245 250 255
 Asn Glu Gln Lys Pro Asn Phe Lys Ile Gly Thr Phe Met Ile Pro Gly
 260 265 270
 Lys Glu Lys Gly Gln Ser Leu Thr Val Gly Ala Gly Asp Leu Ala Trp
 275 280 285
 Ser Ile Ser Ala Thr Thr Lys His Pro Lys Glu Ala Asn Ala Phe Val
 290 295 300
 Glu Tyr Met Thr Arg Pro Glu Val Met Gln Lys Tyr Tyr Asp Val Asp
 305 310 315 320
 Gly Ser Pro Thr Ala Ile Glu Gly Val Lys Gln Ala Gly Glu Asp Ser
 325 330 335
 Pro Leu Ala Gly Met Thr Glu Tyr Ala Phe Thr Asp Arg His Leu Val
 340 345 350

0076321 0330
 T 000000 000000

Trp Leu Gln Gln Tyr Trp Thr Ser Glu Ala Asp Phe His Thr Leu Thr
355 360 365

Met Asn Tyr Val Leu Thr Gly Asp Lys Gln Gly Met Val Asn Asp Leu
370 375 380

Asn Ala Phe Phe Asn Pro Met Lys Ala Asp Val Asp
385 390 395

(2) INFORMATION FOR SEQ ID NO: 17:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 775 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 17:

TGGGAAAAAT TCTAGCGAAA CTAGTGGAGA TAATTGGTCA AAGTACCAGT CTAACAAGTC	60
TATTACTATT GGATTGATA GTACTTTTGT TCCAATGGGA TTTGCTCAGA AAGATGGTTC	120
TTATGCAGGA TTTGATATTG ATTTAGCTAC AGCTGTTTTT GAAAAATACG GAATCACGGT	180
AAATTGGCAA CCGATTGATT GGGATTTGAA AGAAGCTGAA TTGACAAAAG GAACGATTGA	240
TCTGATTTGG AATGGCTATT CCGCTACAGA CGAACGCCGT GAAAAGGTGG CTTTCAGTAA	300
CTCATATATG AAGAATGAGC AGGTATTGGT TACGAAGAAA TCATCTGGTA TCACGACTGC	360
AAAGGATATG ACTGGAAAGA CATTAGGAGC TCAAGCTGGT TCATCTGGTT ATGCGGACTT	420
TGAAGCAAAT CCAGAAATTT TGAAGAATAT TGTCGCTAAT AAGGAAGCGA ATCAATACCA	480
AACCTTTAAT GAAGCCTTGA TTGATTTGAA AAACGATCGA ATTGATGGTC TATTGATTGA	540
CCGTGTCTAT GCAAACCTATT ATTTAGAAGC AGAAGGTGTT TTAAACGATT ATAATGTCTT	600
TACAGTTGGA CTAGAAACAG AAGCTTTTGC GGTGAGGCC CGTAAGGAAG ATACAACTT	660
GGTTAAGAAG ATAAATGAAG CTTTTTCTAG TCTTTACAAG GACGGCAAGT TCCAAGAAAT	720
CAGCCAAAAA TGGTTTGGAG AAGATGTAGC AACCAAAGAA GTAAAAGAAG GACAG	775

(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 258 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

Gly Lys Asn Ser Ser Glu Thr Ser Gly Asp Asn Trp Ser Lys Tyr Gln
1 5 10 15
Ser Asn Lys Ser Ile Thr Ile Gly Phe Asp Ser Thr Phe Val Pro Met

131

20

25

30

Gly Phe Ala Gln Lys Asp Gly Ser Tyr Ala Gly Phe Asp Ile Asp Leu
 35 40 45
 Ala Thr Ala Val Phe Glu Lys Tyr Gly Ile Thr Val Asn Trp Gln Pro
 50 55 60
 Ile Asp Trp Asp Leu Lys Glu Ala Glu Leu Thr Lys Gly Thr Ile Asp
 65 70 75 80
 Leu Ile Trp Asn Gly Tyr Ser Ala Thr Asp Glu Arg Arg Glu Lys Val
 85 90 95
 Ala Phe Ser Asn Ser Tyr Met Lys Asn Glu Gln Val Leu Val Thr Lys
 100 105 110
 Lys Ser Ser Gly Ile Thr Thr Ala Lys Asp Met Thr Gly Lys Thr Leu
 115 120 125
 Gly Ala Gln Ala Gly Ser Ser Gly Tyr Ala Asp Phe Glu Ala Asn Pro
 130 135 140
 Glu Ile Leu Lys Asn Ile Val Ala Asn Lys Glu Ala Asn Gln Tyr Gln
 145 150 155 160
 Thr Phe Asn Glu Ala Leu Ile Asp Leu Lys Asn Asp Arg Ile Asp Gly
 165 170 175
 Leu Leu Ile Asp Arg Val Tyr Ala Asn Tyr Tyr Leu Glu Ala Glu Gly
 180 185 190
 Val Leu Asn Asp Tyr Asn Val Phe Thr Val Gly Leu Glu Thr Glu Ala
 195 200 205
 Phe Ala Val Gly Ala Arg Lys Glu Asp Thr Asn Leu Val Lys Lys Ile
 210 215 220
 Asn Glu Ala Phe Ser Ser Leu Tyr Lys Asp Gly Lys Phe Gln Glu Ile
 225 230 235 240
 Ser Gln Lys Trp Phe Gly Glu Asp Val Ala Thr Lys Glu Val Lys Glu
 245 250 255
 Gly Gln

(2) INFORMATION FOR SEQ ID NO: 19:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 868 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 19:

TGCTAGCGGA AAAAAAGATA CAACTTCTGG TCAAAACTA AAAGTTGTTG CTACAAACTC

60

AATCATCGCT GATATTACTA AAAATATTGC TGGTGACAAA ATTGACCTTC ATAGTATCGT

120

TCCGATTGGG CAAGACCCAC ACGAATACGA ACCACTTCCT GAAGACGTTA AGAAAACTTC 180
 TGAGGCTAAT TTGATTTTCT ATAACGGTAT CAACCTTGAA ACAGGTGGCA ATGCTTGTT 240
 TACAAAATTG GTAGAAAATG CCAAGAAAAC TGAAAACAAA GACTACTTCG CAGTCAGCGA 300
 CGGCGTTGAT GTTATCTACC TTGAAGGTCA AAATGAAAAA GGAAAAGAAG ACCCACACGC 360
 TTGGCTTAAC CTTGAAAACG GTATTATTTT TGCTAAAAAT ATCGCCAAAC AATTGAGCGC 420
 CAAAGACCCT AACAATAAAG AATTCTATGA AAAAAATCTC AAAGAATATA CTGATAAGTT 480
 AGACAACTT GATAAAGAAA GTAAGGATAA ATTTAATAAG ATCCCTGCTG AAAAGAAACT 540
 CATTGTAACC AGCGAAGGAG CATTCAAATA CTTCTCTAAA GCCTATGGTG TCCCAAGTGC 600
 TTACATCTGG GAAATCAATA CTGAAGAAGA AGGAACTCCT GAACAAATCA AGACCTTGGT 660
 TGAAAACTT CGCCAAACAA AAGTTCCATC ACTCTTTGTA GAATCAAGTG TGGATGACCG 720
 TCCAATGAAA ACTGTTTCTC AAGACACAAA CATCCCAATC TACGCTCAAA TCTTTACTGA 780
 CTCTATCGCA GAACAAGGTA AAGAAGGCGA CAGCTACTAC AGCATGATGA AATACAACCT 840
 TGACAAGATT GCTGAAGGAT TGGCAAAA 868

(2) INFORMATION FOR SEQ ID NO:20:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 289 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

Ala Ser Gly Lys Lys Asp Thr Thr Ser Gly Gln Lys Leu Lys Val Val
 1 5 10 15
 Ala Thr Asn Ser Ile Ile Ala Asp Ile Thr Lys Asn Ile Ala Gly Asp
 20 25 30
 Lys Ile Asp Leu His Ser Ile Val Pro Ile Gly Gln Asp Pro His Glu
 35 40 45
 Tyr Glu Pro Leu Pro Glu Asp Val Lys Lys Thr Ser Glu Ala Asn Leu
 50 55 60
 Ile Phe Tyr Asn Gly Ile Asn Leu Glu Thr Gly Gly Asn Ala Trp Phe
 65 70 75 80
 Thr Lys Leu Val Glu Asn Ala Lys Lys Thr Glu Asn Lys Asp Tyr Phe
 85 90 95
 Ala Val Ser Asp Gly Val Asp Val Ile Tyr Leu Glu Gly Gln Asn Glu
 100 105 110
 Lys Gly Lys Glu Asp Pro His Ala Trp Leu Asn Leu Glu Asn Gly Ile
 115 120 125

Ile Phe Ala Lys Asn Ile Ala Lys Gln Leu Ser Ala Lys Asp Pro Asn
 130 135 140
 Asn Lys Glu Phe Tyr Glu Lys Asn Leu Lys Glu Tyr Thr Asp Lys Leu
 145 150 155 160
 Asp Lys Leu Asp Lys Glu Ser Lys Asp Lys Phe Asn Lys Ile Pro Ala
 165 170 175
 Glu Lys Lys Leu Ile Val Thr Ser Glu Gly Ala Phe Lys Tyr Phe Ser
 180 185 190
 Lys Ala Tyr Gly Val Pro Ser Ala Tyr Ile Trp Glu Ile Asn Thr Glu
 195 200 205
 Glu Glu Gly Thr Pro Glu Gln Ile Lys Thr Leu Val Glu Lys Leu Arg
 210 215 220
 Gln Thr Lys Val Pro Ser Leu Phe Val Glu Ser Ser Val Asp Asp Arg
 225 230 235 240
 Pro Met Lys Thr Val Ser Gln Asp Thr Asn Ile Pro Ile Tyr Ala Gln
 245 250 255
 Ile Phe Thr Asp Ser Ile Ala Glu Gln Gly Lys Glu Gly Asp Ser Tyr
 260 265 270
 Tyr Ser Met Met Lys Tyr Asn Leu Asp Lys Ile Ala Glu Gly Leu Ala
 275 280 285

Lys

(2) INFORMATION FOR SEQ ID NO: 21:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1546 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 21:

TGGCTCAAAA AATACAGCTT CAAGTCCAGA TTATAAGTTG GAAGGTGTAA CATTCCCGCT	60
TCAAGAAAAG AAAACATTGA AGTTTATGAC AGCCAGTTCA CCGTTATCTC CTAAAGACCC	120
AAATGAAAAG TTAATTTTGC AACGTTTGGG GAAGGAAACT GCGGTCATA TTGACTGGAC	180
CAACTACCAA TCCGACTTTG CAGAAAAACG TAACTTGGAT ATTTCTAGTG GTGATTTACC	240
AGATGCTATC CACAACGACG GAGCTTCAGA TGTGGACTTG ATGAACTGGG CTAAAAAAGG	300
TGTTATTATT CCAGTTGAAG ATTTGATTGA TAAATACATG CCAAATCTTA AGAAAATTTT	360
GGATGAGAAA CCAGAGTACA AGGCCTTGAT GACAGCACCT GATGGGCACA TTTACTCATT	420
TCCATGGATT GAAGAGCTTG GAGATGGTAA AGAGTCTATT CACAGTGTC ACGATATGGC	480
TTGGATTAAC AAAGATTGGC TTAAGAAACT TGGTCTTGAA ATGCCAAAAA CTA CTGATGA	540

TTTGATTAAA GTCCTAGAAG CTTTCAAAAA CGGGGATCCA AATGGAAATG GAGAGGCTGA 600
 TGAAATTCCA TTTTCATTTA TTAGTGGTAA CGGAAACGAA GATTTTAAAT TCCTATTTGC 660
 TGCATTTGGT ATAGGGGATA ACGATGATCA TTTAGTAGTA GGAAATGATG GCAAAGTTGA 720
 CTTACACAGCA GATAACGATA ACTATAAAGA AGGTGTCAAA TTTATCCGTC AATTGCAAGA 780
 AAAAGGCCTG ATTGATAAAG AAGCTTTTCGA ACATGATTGG AATAGTTACA TTGCTAAAGG 840
 TCATGATCAG AAATTTGGTG TTTACTTTAC ATGGGATAAG AATAATGTTA CTGGAAGTAA 900
 CGAAAGTTAT GATGTTTTAC CAGTACTTGC TGGACCAAGT GGTCAAAAAC ACGTAGCTCG 960
 TACAAACGGT ATGGGATTTG CACGTGACAA GATGGTTATT ACCAGTGTA AAAAAACCT 1020
 AGAATTGACA GCTAAATGGA TTGATGCACA ATACGCTCCA CTCCAATCTG TGCAAAATAA 1080
 CTGGGGAAC TACGGAGATG ACAAACAACA AAACATCTTT GAATTGGATC AAGCGTCAAA 1140
 TAGTCTAAAA CACTTACCAC TAAACGGAAC TGCACCAGCA GAACTTCGTC AAAAGACTGA 1200
 AGTAGGAGGA CCACTAGCTA TCCTAGATTC ATACTATGGT AAAGTAACAA CCATGCCTGA 1260
 TGATGCCAAA TGGCGTTTGG ATCTTATCAA AGAATATTAT GTTCCTTACA TGAGCAATGT 1320
 CAATAACTAT CCAAGAGTCT TTATGACACA GGAAGATTTG GACAAGATTG CCCATATCGA 1380
 AGCAGATATG AATGACTATA TCTACCGTAA ACGTGCTGAA TGGATTGTAA ATGGCAATAT 1440
 TGATACTGAG TGGGATGATT ACAAGAAAGA ACTTGAAAAA TACGGACTTT CTGATTACCT 1500
 CGCTATTAAA CAAAATACT ACGACCAATA CCAAGCAAAC AAAAAC 1546

(2) INFORMATION FOR SEQ ID NO:22:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 515 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

Gly Ser Lys Asn Thr Ala Ser Ser Pro Asp Tyr Lys Leu Glu Gly Val
 1 5 10 15
 Thr Phe Pro Leu Gln Glu Lys Lys Thr Leu Lys Phe Met Thr Ala Ser
 20 25 30
 Ser Pro Leu Ser Pro Lys Asp Pro Asn Glu Lys Leu Ile Leu Gln Arg
 35 40 45
 Leu Glu Lys Glu Thr Gly Val His Ile Asp Trp Thr Asn Tyr Gln Ser
 50 55 60
 Asp Phe Ala Glu Lys Arg Asn Leu Asp Ile Ser Ser Gly Asp Leu Pro
 65 70 75 80
 Asp Ala Ile His Asn Asp Gly Ala Ser Asp Val Asp Leu Met Asn Trp

135

85

90

95

Ala	Lys	Lys	Gly	Val	Ile	Ile	Pro	Val	Glu	Asp	Leu	Ile	Asp	Lys	Tyr
			100					105					110		
Met	Pro	Asn	Leu	Lys	Lys	Ile	Leu	Asp	Glu	Lys	Pro	Glu	Tyr	Lys	Ala
		115					120					125			
Leu	Met	Thr	Ala	Pro	Asp	Gly	His	Ile	Tyr	Ser	Phe	Pro	Trp	Ile	Glu
	130					135					140				
Glu	Leu	Gly	Asp	Gly	Lys	Glu	Ser	Ile	His	Ser	Val	Asn	Asp	Met	Ala
145					150					155					160
Trp	Ile	Asn	Lys	Asp	Trp	Leu	Lys	Lys	Leu	Gly	Leu	Glu	Met	Pro	Lys
				165					170					175	
Thr	Thr	Asp	Asp	Leu	Ile	Lys	Val	Leu	Glu	Ala	Phe	Lys	Asn	Gly	Asp
			180					185					190		
Pro	Asn	Gly	Asn	Gly	Glu	Ala	Asp	Glu	Ile	Pro	Phe	Ser	Phe	Ile	Ser
		195					200					205			
Gly	Asn	Gly	Asn	Glu	Asp	Phe	Lys	Phe	Leu	Phe	Ala	Ala	Phe	Gly	Ile
	210					215					220				
Gly	Asp	Asn	Asp	Asp	His	Leu	Val	Val	Gly	Asn	Asp	Gly	Lys	Val	Asp
225					230					235					240
Phe	Thr	Ala	Asp	Asn	Asp	Asn	Tyr	Lys	Glu	Gly	Val	Lys	Phe	Ile	Arg
				245					250					255	
Gln	Leu	Gln	Glu	Lys	Gly	Leu	Ile	Asp	Lys	Glu	Ala	Phe	Glu	His	Asp
			260					265					270		
Trp	Asn	Ser	Tyr	Ile	Ala	Lys	Gly	His	Asp	Gln	Lys	Phe	Gly	Val	Tyr
		275					280					285			
Phe	Thr	Trp	Asp	Lys	Asn	Asn	Val	Thr	Gly	Ser	Asn	Glu	Ser	Tyr	Asp
	290					295					300				
Val	Leu	Pro	Val	Leu	Ala	Gly	Pro	Ser	Gly	Gln	Lys	His	Val	Ala	Arg
305					310					315					320
Thr	Asn	Gly	Met	Gly	Phe	Ala	Arg	Asp	Lys	Met	Val	Ile	Thr	Ser	Val
				325					330					335	
Asn	Lys	Asn	Leu	Glu	Leu	Thr	Ala	Lys	Trp	Ile	Asp	Ala	Gln	Tyr	Ala
			340					345					350		
Pro	Leu	Gln	Ser	Val	Gln	Asn	Asn	Trp	Gly	Thr	Tyr	Gly	Asp	Asp	Lys
		355					360					365			
Gln	Gln	Asn	Ile	Phe	Glu	Leu	Asp	Gln	Ala	Ser	Asn	Ser	Leu	Lys	His
	370					375					380				
Leu	Pro	Leu	Asn	Gly	Thr	Ala	Pro	Ala	Glu	Leu	Arg	Gln	Lys	Thr	Glu
385					390					395					400
Val	Gly	Gly	Pro	Leu	Ala	Ile	Leu	Asp	Ser	Tyr	Tyr	Gly	Lys	Val	Thr
				405					410					415	
Thr	Met	Pro	Asp	Asp	Ala	Lys	Trp	Arg	Leu	Asp	Leu	Ile	Lys	Glu	Tyr

420	425	430
Tyr Val Pro Tyr Met Ser Asn	Val Asn Asn Tyr Pro Arg Val Phe Met	
435	440	445
Thr Gln Glu Asp Leu Asp Lys	Ile Ala His Ile Glu Ala Asp Met Asn	
450	455	460
Asp Tyr Ile Tyr Arg Lys Arg	Ala Glu Trp Ile Val Asn Gly Asn Ile	
465	470	475
Asp Thr Glu Trp Asp Asp Tyr	Lys Lys Glu Leu Glu Lys Tyr Gly Leu	
485	490	495
Ser Asp Tyr Leu Ala Ile Lys	Gln Lys Tyr Tyr Asp Gln Tyr Gln Ala	
500	505	510
Asn Lys Asn		
515		

(2) INFORMATION FOR SEQ ID NO: 23:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 895 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 23:

TAGTACAAAC TCAAGCACTA GTCAGACAGA GACCAGTAGC TCTGCTCCAA CAGAGGTAAC	60
CATTAAAGT TCACTGGACG AGGTCAAAC TCCAAAGTT CCTGAAAAGA TTGTGACCTT	120
TGACCTCGGC GCTGCGGATA CTATTCGCGC TTTAGGATTT GAAAAAATA TCGTCGGAAT	180
GCCTACAAAA ACTGTTCCGA CTTATCTAAA AGACCTAGTG GGAAGTGTCA AAAATGTTGG	240
TTCTATGAAA GAACCTGATT TAGAAGCTAT CGCCGCCCTT GAGCCTGATT TGATTATCGC	300
TTCGCCACGT ACACAAAAAT TCGTAGACAA ATTCAAAGAA ATCGCCCCAA CCGTTCTCTT	360
CCAAGCAAGC AAGGACGACT ACTGGACTTC TACCAAGGCT AATATCGAAT CCTTAGCAAG	420
TGCCTTCGGC GAAACTGGTA CACAGAAAGC CAAGGAAGAA TTGACCAAGC TAGACAAGAG	480
CATCCAAGAA GTCGCTACTA AAAATGAAAG CTCTGACAAA AAAGCCCTTG CGATCCTCCT	540
TAATGAAGGA AAAATGGCAG CCTTTGGTGC CAAATCTCGT TTCTCTTTCT TGTACCAAAC	600
CTTGAAATTC AAACCAACTG ATACAAAATT TGAAGACTCA CGCCACGGAC AAGAAGTCAG	660
CTTTGAAAGT GTCAAAGAAA TCAACCCTGA CATCCTCTTT GTCATCAACC GTACCCTTGC	720
CATCGGTGGG GACAACTCTA GCAACGACGG TGTCCTAGAA AATGCCCTTA TCGCTGAAAC	780
ACCTGCTGCT AAAAATGGTA AGATTATCCA ACTAACACCA GACCTCTGGT ATCTAAGCGG	840
AGGCGGACTT GAATCAACAA AACTCATGAT TGAAGACATA CAAAAGCTT TGAAA	895

(2) INFORMATION FOR SEQ ID NO: 24:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 298 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

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Ser Thr Asn Ser Ser Thr Ser Gln Thr Glu Thr Ser Ser Ser Ala Pro
1      5      10
Thr Glu Val Thr Ile Lys Ser Ser Leu Asp Glu Val Lys Leu Ser Lys
20    25    30
Val Pro Glu Lys Ile Val Thr Phe Asp Leu Gly Ala Ala Asp Thr Ile
35    40    45
Arg Ala Leu Gly Phe Glu Lys Asn Ile Val Gly Met Pro Thr Lys Thr
50    55    60
Val Pro Thr Tyr Leu Lys Asp Leu Val Gly Thr Val Lys Asn Val Gly
65    70    75    80
Ser Met Lys Glu Pro Asp Leu Glu Ala Ile Ala Ala Leu Glu Pro Asp
85    90    95
Leu Ile Ile Ala Ser Pro Arg Thr Gln Lys Phe Val Asp Lys Phe Lys
100   105   110
Glu Ile Ala Pro Thr Val Leu Phe Gln Ala Ser Lys Asp Asp Tyr Trp
115   120   125
Thr Ser Thr Lys Ala Asn Ile Glu Ser Leu Ala Ser Ala Phe Gly Glu
130   135   140
Thr Gly Thr Gln Lys Ala Lys Glu Glu Leu Thr Lys Leu Asp Lys Ser
145   150   155   160
Ile Gln Glu Val Ala Thr Lys Asn Glu Ser Ser Asp Lys Lys Ala Leu
165   170   175
Ala Ile Leu Leu Asn Glu Gly Lys Met Ala Ala Phe Gly Ala Lys Ser
180   185   190
Arg Phe Ser Phe Leu Tyr Gln Thr Leu Lys Phe Lys Pro Thr Asp Thr
195   200   205
Lys Phe Glu Asp Ser Arg His Gly Gln Glu Val Ser Phe Glu Ser Val
210   215   220
Lys Glu Ile Asn Pro Asp Ile Leu Phe Val Ile Asn Arg Thr Leu Ala
225   230   235   240
Ile Gly Gly Asp Asn Ser Ser Asn Asp Gly Val Leu Glu Asn Ala Leu
245   250   255
Ile Ala Glu Thr Pro Ala Ala Lys Asn Gly Lys Ile Ile Gln Leu Thr
260   265   270

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Pro Asp Leu Trp Tyr Leu Ser Gly Gly Gly Leu Glu Ser Thr Lys Leu
 275 280 285

Met Ile Glu Asp Ile Gln Lys Ala Leu Lys
 290 295

(2) INFORMATION FOR SEQ ID NO: 25:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1261 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 25:

TGGCAATTCT GGCGGAAGTA AAGATGCTGC CAAATCAGGT GGTGACGGTG CCAAAACAGA	60
AATCACTTGG TGGGCATTCC CAGTATTTAC CCAAGAAAAA ACTGGTGACG GTGTTGGAAC	120
TTATGAAAAA TCAATCATCG AAGCGTTTGA AAAAGCAAAC CCAGATATAA AAGTGAAATT	180
GGAAACCATC GACTTCAAGT CAGGTCCTGA AAAAATCACA ACAGCCATCG AAGCAGGAAC	240
AGCTCCAGAC GTACTCTTTG ATGCACCAGG ACGTATCATC CAATACGGTA AAAACGGTAA	300
ATTGGCTGAG TTGAATGACC TCTTCACAGA TGAATTTGTT AAAGATGTCA ACAATGAAAA	360
CATCGTACAA GCAAGTAAAG CTGGAGACAA GGCTTATATG TATCCGATTA GTTCTGCCCC	420
ATTCTACATG GCAATGAACA AGAAAATGTT AGAAGATGCT GGAGTAGCAA ACCTTGTAAG	480
AGAAGGTTGG ACAACTGATG ATTTTGAAAA AGTATTGAAA GCACTTAAAG ACAAGGGTTA	540
CACACCAGGT TCATTGTTCA GTTCTGGTCA AGGGGGAGAC CAAGGAACAC GTGCCTTTAT	600
CTCTAACCTT TATAGCGGTT CTGTAACAGA TGAAAAAGTT AGCAAATATA CAACTGATGA	660
TCCTAAATTC GTCAAAGGTC TTGAAAAAGC AACTAGCTGG ATTAAAGACA ATTTGATCAA	720
TAATGGTTCA CAATTTGACG GTGGGGCAGA TATCCAAAAC TTTGCCAACG GTCAAACATC	780
TTACACAATC CTTTGGGCAC CAGCTCAAAA TGGTATCCAA GCTAAACTTT TAGAAGCAAG	840
TAAGGTAGAA GTGGTAGAAG TACCATTCCC ATCAGACGAA GGTAAGCCAG CTCTTGAGTA	900
CCTTGTAAC GGGTTTGCAG TATTCAACAA TAAAGACGAC AAGAAAGTCG CTGCATCTAA	960
GAAATTCATC CAGTTTATCG CAGATGACAA GGAGTGGGGA CCTAAAGACG TAGTTCGTAC	1020
AGGTGCTTTC CCAGTCCGTA CTTCAATTTGG AAAACTTTAT GAAGACAAAC GCATGGAAAC	1080
AATCAGCGGC TGGACTCAAT ACTACTCACC ATACTACAAC ACTATTGATG GATTGCTGA	1140
AATGAGAACA CTTTGGTTCC CAATGTTGCA ATCTGTATCA AATGGTGACG AAAAACCAGC	1200
AGATGCTTTG AAAGCCTTCA CTGAAAAAGC GAACGAAACA ATCAAAAAAG CTATGAAACA	1260
A	1261

(2) INFORMATION FOR SEQ ID NO:26:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 420 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

Gly Asn Ser Gly Gly Ser Lys Asp Ala Ala Lys Ser Gly Gly Asp Gly
 1 5 10 15
 Ala Lys Thr Glu Ile Thr Trp Trp Ala Phe Pro Val Phe Thr Gln Glu
 20 25 30
 Lys Thr Gly Asp Gly Val Gly Thr Tyr Glu Lys Ser Ile Ile Glu Ala
 35 40 45
 Phe Glu Lys Ala Asn Pro Asp Ile Lys Val Lys Leu Glu Thr Ile Asp
 50 55 60
 Phe Lys Ser Gly Pro Glu Lys Ile Thr Thr Ala Ile Glu Ala Gly Thr
 65 70 75 80
 Ala Pro Asp Val Leu Phe Asp Ala Pro Gly Arg Ile Ile Gln Tyr Gly
 85 90 95
 Lys Asn Gly Lys Leu Ala Glu Leu Asn Asp Leu Phe Thr Asp Glu Phe
 100 105 110
 Val Lys Asp Val Asn Asn Glu Asn Ile Val Gln Ala Ser Lys Ala Gly
 115 120 125
 Asp Lys Ala Tyr Met Tyr Pro Ile Ser Ser Ala Pro Phe Tyr Met Ala
 130 135 140
 Met Asn Lys Lys Met Leu Glu Asp Ala Gly Val Ala Asn Leu Val Lys
 145 150 155 160
 Glu Gly Trp Thr Thr Asp Asp Phe Glu Lys Val Leu Lys Ala Leu Lys
 165 170 175
 Asp Lys Gly Tyr Thr Pro Gly Ser Leu Phe Ser Ser Gly Gln Gly Gly
 180 185 190
 Asp Gln Gly Thr Arg Ala Phe Ile Ser Asn Leu Tyr Ser Gly Ser Val
 195 200 205
 Thr Asp Glu Lys Val Ser Lys Tyr Thr Thr Asp Asp Pro Lys Phe Val
 210 215 220
 Lys Gly Leu Glu Lys Ala Thr Ser Trp Ile Lys Asp Asn Leu Ile Asn
 225 230 235 240
 Asn Gly Ser Gln Phe Asp Gly Gly Ala Asp Ile Gln Asn Phe Ala Asn
 245 250 255
 Gly Gln Thr Ser Tyr Thr Ile Leu Trp Ala Pro Ala Gln Asn Gly Ile
 260 265 270

(2) INFORMATION FOR SEQ ID NO: 27:

(A) LENGTH: 658 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

TTCACAAGAA	AAAACAAAAA	ATGAAGATGG	AGAAACTAAG	ACAGAACAGA	CAGCCAAAGC	60
TGATGGAACA	GTCGGTAGTA	AGTCTCAAGG	AGCTGCCCAG	AAGAAAGCAG	AAGTGGTCAA	120
TAAAGGTGAT	TACTACAGCA	TTCAAGGGAA	ATACGATGAA	ATCATCGTAG	CCAACAAACA	180
CTATCCATTG	TCTAAAGACT	ATAATCCAGG	GGAAAATCCA	ACAGCCAAGG	CAGAGTTGGT	240
CAAACCTCATC	AAAGCGATGC	AAGAGGCAGG	TTTCCCTATT	AGTGATCATT	ACAGTGGTTT	300
TAGAAGTTAT	GAAACTCAGA	CCAAGCTCTA	TCAAGATTAT	GTCAACCAAG	ATGGAAAGGC	360
AGCAGCTGAC	CGTTACTCTG	CCCGTCCTGG	CTATAGCGAA	CACCAGACAG	GCTTGGCCTT	420
TGATGTGATT	GGGACTGATG	GTGATTTGGT	GACAGAAGAA	AAAGCAGCCC	AATGGCTCTT	480
GGATCATGCA	GCTGATTATG	GCTTTGTTGT	CCGTTATCTC	AAAGGCAAGG	AAAAGGAAAC	540
AGGCTATATG	GCTGAAGAAT	GGCACCTGCG	TTATGTAGGA	AAAGAAGCTA	AAGAAATTGC	600
TGCAAGTGGT	CTCAGTTTGG	AAGAATACTA	TGGCTTTGAA	GGCGGAGACT	ACGTCGAT	658

(2) INFORMATION FOR SEQ ID NO:28:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 219 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

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Ser  Gln  Glu  Lys  Thr  Lys  Asn  Glu  Asp  Gly  Glu  Thr  Lys  Thr  Glu  Gln
1      5      10      15
Thr  Ala  Lys  Ala  Asp  Gly  Thr  Val  Gly  Ser  Lys  Ser  Gln  Gly  Ala  Ala
      20      25      30
Gln  Lys  Lys  Ala  Glu  Val  Val  Asn  Lys  Gly  Asp  Tyr  Tyr  Ser  Ile  Gln
      35      40      45
Gly  Lys  Tyr  Asp  Glu  Ile  Ile  Val  Ala  Asn  Lys  His  Tyr  Pro  Leu  Ser
      50      55      60
Lys  Asp  Tyr  Asn  Pro  Gly  Glu  Asn  Pro  Thr  Ala  Lys  Ala  Glu  Leu  Val
      65      70      75      80
Lys  Leu  Ile  Lys  Ala  Met  Gln  Glu  Ala  Gly  Phe  Pro  Ile  Ser  Asp  His
      85      90      95
Tyr  Ser  Gly  Phe  Arg  Ser  Tyr  Glu  Thr  Gln  Thr  Lys  Leu  Tyr  Gln  Asp
      100     105     110
Tyr  Val  Asn  Gln  Asp  Gly  Lys  Ala  Ala  Ala  Asp  Arg  Tyr  Ser  Ala  Arg
      115     120     125
Pro  Gly  Tyr  Ser  Glu  His  Gln  Thr  Gly  Leu  Ala  Phe  Asp  Val  Ile  Gly
      130     135     140
Thr  Asp  Gly  Asp  Leu  Val  Thr  Glu  Glu  Lys  Ala  Ala  Gln  Trp  Leu  Leu
      145     150     155     160
Asp  His  Ala  Ala  Asp  Tyr  Gly  Phe  Val  Val  Arg  Tyr  Leu  Lys  Gly  Lys
      165     170     175
Glu  Lys  Glu  Thr  Gly  Tyr  Met  Ala  Glu  Glu  Trp  His  Leu  Arg  Tyr  Val
      180     185     190
Gly  Lys  Glu  Ala  Lys  Glu  Ile  Ala  Ala  Ser  Gly  Leu  Ser  Leu  Glu  Glu
      195     200     205
Tyr  Tyr  Gly  Phe  Glu  Gly  Gly  Asp  Tyr  Val  Asp
      210     215

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(2) INFORMATION FOR SEQ ID NO: 29:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 790 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 29:

GAAAGGTCTG TGGTCAAATA ATCTTACCTG CGGTTATGAT GAAAAAATAA TCTTGAAAA 60
 TATAAATATA AAAATACCTG AAGAAAAAAT ATCAGTTATT ATTGGGTCAA ATGTTTGTGG 120
 GAAATCAACA CTCATTAAAA CCTTGTCTCG ACTTATAAAG CCATTAGAGG GAGAAGTATT 180
 GCTTGATAAT AAATCAATTA ATTCTTATAA AGAAAAAGAT TTAGCAAAAC ACATAGCTAT 240
 ATTACCTCAA TCTCCAATAA TCCCTGAATC AATAACAGTA GCTGATCTTG TAAGCCGTGG 300
 TCGTTTCCCC TACAGAAAGC CTTTAAAGAG TCTTGAAAA GATGACCTTG AAATAATAAA 360
 CAGATCAATG GTTAAGGCCA ATGTTGAAGA TCTAGCAAAT AACCTAGTTG AAGAACTTTC 420
 TGGGGGTCAA AGGCAAAGAG TATGGATAGC TCTAGCCCTA GCCCAAGATA CAAGTATCCT 480
 ACTTTTAGAT GAGCCAACTA CTTACTTGA TATCTCATAT CAAATAGAAC TATTAGACCT 540
 CTTGACTGAT CTAAACCAAA AATATAAGAC AACCATTGTC ATGATTTTGC ACGATATAAA 600
 TCTAACAGCA AGATACGCTG ATTACCTATT TGCAATTAAA GAAGGTAAAC TTGTTGCAGA 660
 GGGAAAGCCT GAAGATATAC TAAATGATAA ACTAGTTAAA GATATCTTTA ATCTTGAAGC 720
 AAAAATTATA CGTGACCCTA TTTCCAATTC GCCTCTAATG ATTCCTATTG GCAAGCACCA 780
 TGTTAACCTCT 790

(2) INFORMATION FOR SEQ ID NO:30:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 262 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

Lys Gly Leu Trp Ser Asn Asn Leu Thr Cys Gly Tyr Asp Glu Lys Ile
 1 5 10 15
 Ile Leu Glu Asn Ile Asn Ile Lys Ile Pro Glu Glu Lys Ile Ser Val
 20 25 30
 Ile Ile Gly Ser Asn Gly Cys Gly Lys Ser Thr Leu Ile Lys Thr Leu
 35 40 45
 Ser Arg Leu Ile Lys Pro Leu Glu Gly Glu Val Leu Leu Asp Asn Lys
 50 55 60
 Ser Ile Asn Ser Tyr Lys Glu Lys Asp Leu Ala Lys His Ile Ala Ile
 65 70 75 80
 Leu Pro Gln Ser Pro Ile Ile Pro Glu Ser Ile Thr Val Ala Asp Leu
 85 90 95

— Val Ser Arg Gly Arg Phe Pro Tyr Arg Lys Pro Phe Lys Ser Leu Gly
 100 105 110
 Lys Asp Asp Leu Glu Ile Ile Asn Arg Ser Met Val Lys Ala Asn Val
 115 120 125
 Glu Asp Leu Ala Asn Asn Leu Val Glu Glu Leu Ser Gly Gly Gln Arg
 130 135 140
 Gln Arg Val Trp Ile Ala Leu Ala Leu Ala Gln Asp Thr Ser Ile Leu
 145 150 155 160
 Leu Leu Asp Glu Pro Thr Thr Tyr Leu Asp Ile Ser Tyr Gln Ile Glu
 165 170 175
 Leu Leu Asp Leu Leu Thr Asp Leu Asn Gln Lys Tyr Lys Thr Thr Ile
 180 185 190
 Cys Met Ile Leu His Asp Ile Asn Leu Thr Ala Arg Tyr Ala Asp Tyr
 195 200 205
 Leu Phe Ala Ile Lys Glu Gly Lys Leu Val Ala Glu Gly Lys Pro Glu
 210 215 220
 Asp Ile Leu Asn Asp Lys Leu Val Lys Asp Ile Phe Asn Leu Glu Ala
 225 230 235 240
 Lys Ile Ile Arg Asp Pro Ile Ser Asn Ser Pro Leu Met Ile Pro Ile
 245 250 255
 Gly Lys His His Val Ser
 260

(2) INFORMATION FOR SEQ ID NO: 31:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 781 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 31:

AAACTCAGAA AAGAAAGCAG ACAATGCAAC AACTATCAAA ATCGCAACTG TTAACCGTAG	60
CGGTTCTGAA GAAAAACGTT GGGACAAAAT CCAAGAATTG GTTAAAAAAG ACGGAATTAC	120
CTTGGAATTT ACAGAGTTCA CAGACTACTC ACAACCAAAC AAAGCAACTG CTGATGGCGA	180
AGTAGATTTG AACGCTTTCC AACACTATAA CTTCTTGAAC AACTGGAACA AAGAAAACGG	240
AAAAGACCTT GTAGCGATTG CAGATACTTA CATCTCTCCA ATCCGCCTTT ACTCAGGTTT	300
GAATGGAAGT GCCAACAAGT AACTAAAGT AGAAGACATC CCAGCAAACG GAGAAATCGC	360
TGTACCGAAT GACGCTACAA ACGAAAGCCG TGCGCTTTAT TTGCTTCAAT CAGCTGGCTT	420
GATTAAATTG GATGTTTCTG GAACTGCTCT TGCAACAGTT GCCAACATCA AAGAAAATCC	480
AAAGAACTTG AAAATCACTG AATTGGACGC TAGCCAAACA GTCGTTCAT TGTCATCAGT	540

TGACGCTGCC GTTGTAACA ATACCTTCGT TACAGAAGCA AAATTGGACT ACAAGAAATC 600
 ACTTTTCAAA GAACAAGCTG ATGAAAAC TC AAAACAATGG TACAACATCA TTGTTGCAAA 660
 AAAAGATTGG GAAACATCAC CTAAGGCTGA TGCTATCAAG AAAGTAATCG CAGCTTACCA 720
 CACAGATGAC GTGAAAAAAG TTATCGAAGA ATCATCAGAT GGT TTGGATC AACCAGTTTG 780
 G 781

(2) INFORMATION FOR SEQ ID NO:32:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 260 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

Asn Ser Glu Lys Lys Ala Asp Asn Ala Thr Thr Ile Lys Ile Ala Thr
 1 5 10 15
 Val Asn Arg Ser Gly Ser Glu Glu Lys Arg Trp Asp Lys Ile Gln Glu
 20 25 30
 Leu Val Lys Lys Asp Gly Ile Thr Leu Glu Phe Thr Glu Phe Thr Asp
 35 40 45
 Tyr Ser Gln Pro Asn Lys Ala Thr Ala Asp Gly Glu Val Asp Leu Asn
 50 55 60
 Ala Phe Gln His Tyr Asn Phe Leu Asn Asn Trp Asn Lys Glu Asn Gly
 65 70 75 80
 Lys Asp Leu Val Ala Ile Ala Asp Thr Tyr Ile Ser Pro Ile Arg Leu
 85 90 95
 Tyr Ser Gly Leu Asn Gly Ser Ala Asn Lys Tyr Thr Lys Val Glu Asp
 100 105 110
 Ile Pro Ala Asn Gly Glu Ile Ala Val Pro Asn Asp Ala Thr Asn Glu
 115 120 125
 Ser Arg Ala Leu Tyr Leu Leu Gln Ser Ala Gly Leu Ile Lys Leu Asp
 130 135 140
 Val Ser Gly Thr Ala Leu Ala Thr Val Ala Asn Ile Lys Glu Asn Pro
 145 150 155 160
 Lys Asn Leu Lys Ile Thr Glu Leu Asp Ala Ser Gln Thr Ala Arg Ser
 165 170 175
 Leu Ser Ser Val Asp Ala Ala Val Val Asn Asn Thr Phe Val Thr Glu
 180 185 190
 Ala Lys Leu Asp Tyr Lys Lys Ser Leu Phe Lys Glu Gln Ala Asp Glu
 195 200 205

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Asn Ser Lys Gln Trp Tyr Asn Ile Ile Val Ala Lys Lys Asp Trp Glu
210 215 220

Thr Ser Pro Lys Ala Asp Ala Ile Lys Lys Val Ile Ala Ala Tyr His
225 230 235 240

Thr Asp Asp Val Lys Lys Val Ile Glu Glu Ser Ser Asp Gly Leu Asp
245 250 255

Gln Pro Val Trp
260

(2) INFORMATION FOR SEQ ID NO: 33:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 640 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 33:

TTCGAAAGGG TCAGAAGGTG CAGACCTTAT CAGCATGAAA GGGGATGTCA TTACAGAACA	60
TCAATTTTAT GAGCAAGTGA AAAGCAACCC TTCAGCCCAA CAAGTCTTGT TAAATATGAC	120
CATCCAAAAA GTTTTTGAAA AACAATATGG CTCAGAGCTT GATGATAAAG AGGTTGATGA	180
TACTATTGCC GAAGAAAAAA AACAATATGG CGAAACTAC CAACGTGTCT TGTCACAAGC	240
AGGTATGACT CTTGAAACAC GTAAAGCTCA AATTCGTACA AGTAAATTAG TTGAGTTGGC	300
AGTTAAGAAG GTAGCAGAAG CTGAATTGAC AGATGAAGCC TATAAGAAAG CCTTTGATGA	360
GTACACTCCA GATGTAACGG CTCAAATCAT CCGTCTTAAT AATGAAGATA AGGCCAAAGA	420
AGTTCTCGAA AAAGCCAAGG CAGAAGGTGC TGATTTTGCT CAATTAGCCA AAGATAATTC	480
AACTGATGAA AAAACAAAAG AAAATGGTGG AGAAATTACC TTTGATTCTG CTTCAACAGA	540
AGTACCTGGA GCAAGTCCAA AAAAGCCGCT TTTGCTTTT AGATGTGGGA TGGTGTCTTCT	600
GGATGTGGAT TACAGCAACT GGGGCACACC AAGCCTACAG	640

(2) INFORMATION FOR SEQ ID NO:34:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 213 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

Ser Lys Gly Ser Glu Gly Ala Asp Leu Ile Ser Met Lys Gly Asp Val
1 5 10 15
Ile Thr Glu His Gln Phe Tyr Glu Gln Val Lys Ser Asn Pro Ser Ala

146

20

25

30

Gln Gln Val Leu Leu Asn Met Thr Ile Gln Lys Val Phe Glu Lys Gln
 35 40 45
 Tyr Gly Ser Glu Leu Asp Asp Lys Glu Val Asp Asp Thr Ile Ala Glu
 50 55 60
 Glu Lys Lys Gln Tyr Gly Glu Asn Tyr Gln Arg Val Leu Ser Gln Ala
 65 70 75 80
 Gly Met Thr Leu Glu Thr Arg Lys Ala Gln Ile Arg Thr Ser Lys Leu
 85 90 95
 Val Glu Leu Ala Val Lys Lys Val Ala Glu Ala Glu Leu Thr Asp Glu
 100 105 110
 Ala Tyr Lys Lys Ala Phe Asp Glu Tyr Thr Pro Asp Val Thr Ala Gln
 115 120 125
 Ile Ile Arg Leu Asn Asn Glu Asp Lys Ala Lys Glu Val Leu Glu Lys
 130 135 140
 Ala Lys Ala Glu Gly Ala Asp Phe Ala Gln Leu Ala Lys Asp Asn Ser
 145 150 155 160
 Thr Asp Glu Lys Thr Lys Glu Asn Gly Gly Glu Ile Thr Phe Asp Ser
 165 170 175
 Ala Ser Thr Glu Val Pro Gly Ala Ser Pro Lys Lys Pro Leu Phe Ala
 180 185 190
 Phe Arg Cys Gly Met Val Phe Leu Asp Val Asp Tyr Ser Asn Trp Gly
 195 200 205
 Thr Pro Ser Leu Gln
 210

(2) INFORMATION FOR SEQ ID NO: 35:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 631 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 35:

GGGGATGGCA GCTTTTAAAA ATCCTAACAA TCAATACAAA GCTATTACAA TTGCTCAAAC 60
 TCTAGGTGAT GATGCTTCTT CAGAGGAATT GGCTGGTAGA TATGGTTCTG CTGTTTCAGTG 120
 TACAGAAGTG ACTGCCTCAA ACCTTTCAAC AGTTAAAACT AAAGCTACGG TTGTAGAAAA 180
 ACCACTGAAA GATTTTtagag CGTCTACGTC TGATCAGTCT GGTGGGTGG AATCTAATGG 240
 TAAATGGTAT TTCTATGAGT CTGGTGATGT GAAGACAGGT TGGGTGAAAA CAGATGGTAA 300
 ATGGTACTAT TTGAATGACT TAGGTGTCAT GCAGACTGGA TTTGTAAAAT TTTCTGGTAG 360
 CTGGTATTAC TTGAGCAATT CAGGTGCTAT GTTTACAGGC TGGGGAACAG ATGGTAGCAG 420

ATGGTTCTAC TTTGACGGCT CAGGAGCTAT GAAGACAGGC TGGTACAAGG AAAATGGCAC 480
 TTGGTATTAC CTTGACGAAG CAGGTATCAT GAAGACAGGT TGGTTTAAAG TCGGACCACA 540
 CTGGTACTAT GCCTACGGTT CAGGAGCTTT GGCTGTGAGC ACAACAACAC CAGATGGTTA 600
 CCGTGTAAT GGTAAATGGTG AATGGGTAAA C 631

(2) INFORMATION FOR SEQ ID NO:36:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 210 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

Gly Met Ala Ala Phe Lys Asn Pro Asn Asn Gln Tyr Lys Ala Ile Thr
 1 5 10 15
 Ile Ala Gln Thr Leu Gly Asp Asp Ala Ser Ser Glu Glu Leu Ala Gly
 20 25 30
 Arg Tyr Gly Ser Ala Val Gln Cys Thr Glu Val Thr Ala Ser Asn Leu
 35 40 45
 Ser Thr Val Lys Thr Lys Ala Thr Val Val Glu Lys Pro Leu Lys Asp
 50 55 60
 Phe Arg Ala Ser Thr Ser Asp Gln Ser Gly Trp Val Glu Ser Asn Gly
 65 70 75 80
 Lys Trp Tyr Phe Tyr Glu Ser Gly Asp Val Lys Thr Gly Trp Val Lys
 85 90 95
 Thr Asp Gly Lys Trp Tyr Tyr Leu Asn Asp Leu Gly Val Met Gln Thr
 100 105 110
 Gly Phe Val Lys Phe Ser Gly Ser Trp Tyr Tyr Leu Ser Asn Ser Gly
 115 120 125
 Ala Met Phe Thr Gly Trp Gly Thr Asp Gly Ser Arg Trp Phe Tyr Phe
 130 135 140
 Asp Gly Ser Gly Ala Met Lys Thr Gly Trp Tyr Lys Glu Asn Gly Thr
 145 150 155 160
 Trp Tyr Tyr Leu Asp Glu Ala Gly Ile Met Lys Thr Gly Trp Phe Lys
 165 170 175
 Val Gly Pro His Trp Tyr Tyr Ala Tyr Gly Ser Gly Ala Leu Ala Val
 180 185 190
 Ser Thr Thr Thr Pro Asp Gly Tyr Arg Val Asn Gly Asn Gly Glu Trp
 195 200 205
 Val Asn
 210

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(2) INFORMATION FOR SEQ ID NO: 37:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1360 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 37:

AGACGAGCAA AAAATTAAGC AAGCAGAAGC GGAAGTTGAG AGTAAACAAG CTGAGGCTAC	60
AAGGTTAAAA AAAATCAAGA CAGATCGTGA AGAAGCAGAA GAAGAAGCTA AACGAAGAGC	120
AGATGCTAAA GAGCAAGGTA AACCAAAGGG GCGGGCAAAA CGAGGAGTTC CTGGAGAGCT	180
AGCAACACCT GATAAAAAAG AAAATGATGC GAAGTCTTCA GATTCTAGCG TAGGTGAAGA	240
AACTCTTCCA AGCCCATCCC TGAAACCAGA AAAAAAGGTA GCAGAAGCTG AGAAGAAGGT	300
TGAAGAAGCT AAGAAAAAG CCGAGGATCA AAAAGAAGAA GATCGCCGTA ACTACCCAAC	360
CAATACTTAC AAAACGCTTG AACTTGAAAT TGCTGAGTCC GATGTGGAAG TAAAAAAGC	420
GGAGCTTGAA CTAGTAAAG AGGAAGCTAA GGAACCTCGA AACGAGGAAA AAGTTAAGCA	480
AGCAAAAGCG GAAGTTGAGA GTAAAAAGC TGAGGCTACA AGGTTAGAAA AAATCAAGAC	540
AGATCGTAAA AAAGCAGAAG AAGAAGCTAA ACGAAAAGCA GCAGAAGAAG ATAAAGTTAA	600
AGAAAAACCA GCTGAACAAC CACAACCAGC GCCGGCTCCA AAAGCAGAAA AACCAGCTCC	660
AGCTCCAAAA CCAGAGAATC CAGCTGAACA ACCAAAAGCA GAAAAACCAG CTGATCAACA	720
AGCTGAAGAA GACTATGCTC GTAGATCAGA AGAAGAATAT AATCGCTTGA CTCAACAGCA	780
ACCGCCAAAA ACTGAAAAAC CAGCACAACC ATCTACTCCA AAAACAGGCT GGAAACAAGA	840
AAACGGTATG TGGTACTTCT ACAATACTGA TGGTTCAATG GCGACAGGAT GGCTCCAAAA	900
CAATGGCTCA TGGTACTACC TCAACAGCAA TGGCGCTATG GCGACAGGAT GGCTCCAAAA	960
CAATGGTTCA TGGTACTATC TAAACGCTAA TGGTTCAATG GCAACAGGAT GGCTCCAAAA	1020
CAATGGTTCA TGGTACTACC TAAACGCTAA TGGTTCAATG GCGACAGGAT GGCTCCAATA	1080
CAATGGCTCA TGGTACTACC TAAACGCTAA TGGTTCAATG GCGACAGGAT GGCTCCAATA	1140
CAATGGCTCA TGGTACTACC TAAACGCTAA TGGTGATATG GCGACAGGTT GGGTGAAAGA	1200
TGGAGATACC TGGTACTATC TTGAAGCATC AGGTGCTATG AAAGCAAGCC AATGGTTCAA	1260
AGTATCAGAT AAATGGTACT ATGTCAATGG CTCAGGTGCC CTTGCAGTCA ACACAACTGT	1320
AGATGGCTAT GGAGTCAATG CCAATGGTGA ATGGGTAAAC	1360

(2) INFORMATION FOR SEQ ID NO:38:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 453 amino acids

(B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

Asp	Glu	Gln	Lys	Ile	Lys	Gln	Ala	Glu	Ala	Glu	Val	Glu	Ser	Lys	Gln	1	5	10	15
Ala	Glu	Ala	Thr	Arg	Leu	Lys	Lys	Ile	Lys	Thr	Asp	Arg	Glu	Glu	Ala	20	25	30	
Glu	Glu	Glu	Ala	Lys	Arg	Arg	Ala	Asp	Ala	Lys	Glu	Gln	Gly	Lys	Pro	35	40	45	
Lys	Gly	Arg	Ala	Lys	Arg	Gly	Val	Pro	Gly	Glu	Leu	Ala	Thr	Pro	Asp	50	55	60	
Lys	Lys	Glu	Asn	Asp	Ala	Lys	Ser	Ser	Asp	Ser	Ser	Val	Gly	Glu	Glu	65	70	75	80
Thr	Leu	Pro	Ser	Pro	Ser	Leu	Lys	Pro	Glu	Lys	Lys	Val	Ala	Glu	Ala	85	90	95	
Glu	Lys	Lys	Val	Glu	Glu	Ala	Lys	Lys	Lys	Ala	Glu	Asp	Gln	Lys	Glu	100	105	110	
Glu	Asp	Arg	Arg	Asn	Tyr	Pro	Thr	Asn	Thr	Tyr	Lys	Thr	Leu	Glu	Leu	115	120	125	
Glu	Ile	Ala	Glu	Ser	Asp	Val	Glu	Val	Lys	Lys	Ala	Glu	Leu	Glu	Leu	130	135	140	
Val	Lys	Glu	Glu	Ala	Lys	Glu	Pro	Arg	Asn	Glu	Glu	Lys	Val	Lys	Gln	145	150	155	160
Ala	Lys	Ala	Glu	Val	Glu	Ser	Lys	Lys	Ala	Glu	Ala	Thr	Arg	Leu	Glu	165	170	175	
Lys	Ile	Lys	Thr	Asp	Arg	Lys	Lys	Ala	Glu	Glu	Glu	Ala	Lys	Arg	Lys	180	185	190	
Ala	Ala	Glu	Glu	Asp	Lys	Val	Lys	Glu	Lys	Pro	Ala	Glu	Gln	Pro	Gln	195	200	205	
Pro	Ala	Pro	Ala	Pro	Lys	Ala	Glu	Lys	Pro	Ala	Pro	Ala	Pro	Lys	Pro	210	215	220	
Glu	Asn	Pro	Ala	Glu	Gln	Pro	Lys	Ala	Glu	Lys	Pro	Ala	Asp	Gln	Gln	225	230	235	240
Ala	Glu	Glu	Asp	Tyr	Ala	Arg	Arg	Ser	Glu	Glu	Glu	Tyr	Asn	Arg	Leu	245	250	255	
Thr	Gln	Gln	Gln	Pro	Pro	Lys	Thr	Glu	Lys	Pro	Ala	Gln	Pro	Ser	Thr	260	265	270	
Pro	Lys	Thr	Gly	Trp	Lys	Gln	Glu	Asn	Gly	Met	Trp	Tyr	Phe	Tyr	Asn	275	280	285	

150

Thr Asp Gly Ser Met Ala Thr Gly Trp Leu Gln Asn Asn Gly Ser Trp
290 295 300

Tyr Tyr Leu Asn Ser Asn Gly Ala Met Ala Thr Gly Trp Leu Gln Asn
305 310 315 320

Asn Gly Ser Trp Tyr Tyr Leu Asn Ala Asn Gly Ser Met Ala Thr Gly
325 330 335

Trp Leu Gln Asn Asn Gly Ser Trp Tyr Tyr Leu Asn Ala Asn Gly Ser
340 345 350

Met Ala Thr Gly Trp Leu Gln Tyr Asn Gly Ser Trp Tyr Tyr Leu Asn
355 360 365

Ala Asn Gly Ser Met Ala Thr Gly Trp Leu Gln Tyr Asn Gly Ser Trp
370 375 380

Tyr Tyr Leu Asn Ala Asn Gly Asp Met Ala Thr Gly Trp Val Lys Asp
385 390 395 400

Gly Asp Thr Trp Tyr Tyr Leu Glu Ala Ser Gly Ala Met Lys Ala Ser
405 410 415

Gln Trp Phe Lys Val Ser Asp Lys Trp Tyr Tyr Val Asn Gly Ser Gly
420 425 430

Ala Leu Ala Val Asn Thr Thr Val Asp Gly Tyr Gly Val Asn Ala Asn
435 440 445

Gly Glu Trp Val Asn
450

(2) INFORMATION FOR SEQ ID NO: 39:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 412 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 39:

CTGTGGTGAG GAAGAACTA AAAAGACTCA AGCAGCACAA CAGCCAAAAC AACAAACGAC	60
TGTACAACAA ATTGCTGTTG GAAAAGATGC TCCAGACTTC ACATTGCAAT CCATGGATGG	120
CAAAGAAGTT AAGTTATCTG ATTTTAAGGG TAAAAAGGTT TACTTGAAGT TTTGGGCTTC	180
ATGGTGTGGT CCATGCAAGA AAAGTATGCC AGAGTTGATG GAACTAGCGG CGAAACCAGA	240
TCGTGATTTC GAAATTCTTA CTGTCATTGC ACCAGGAATT CAAGGTGAAA AAAGTGTGTA	300
GCAATTCCCA CAATGGTTCC AGGAACAAGG ATATAAGGAT ATCCCAGTTC TTTATGATAC	360
CAAAGCAACC ACTTCCAAGC TTATCAAATT CGAAGCATTC CTACAGAATA TT	412

(2) INFORMATION FOR SEQ ID NO:40:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 137 amino acids

- (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:

Cys Gly Glu Glu Glu Thr Lys Lys Thr Gln Ala Ala Gln Gln Pro Lys
 1 5 10 15
 Gln Gln Thr Thr Val Gln Gln Ile Ala Val Gly Lys Asp Ala Pro Asp
 20 25 30
 Phe Thr Leu Gln Ser Met Asp Gly Lys Glu Val Lys Leu Ser Asp Phe
 35 40 45
 Lys Gly Lys Lys Val Tyr Leu Lys Phe Trp Ala Ser Trp Cys Gly Pro
 50 55 60
 Cys Lys Lys Ser Met Pro Glu Leu Met Glu Leu Ala Ala Lys Pro Asp
 65 70 75 80
 Arg Asp Phe Glu Ile Leu Thr Val Ile Ala Pro Gly Ile Gln Gly Glu
 85 90 95
 Lys Thr Val Glu Gln Phe Pro Gln Trp Phe Gln Glu Gln Gly Tyr Lys
 100 105 110
 Asp Ile Pro Val Leu Tyr Asp Thr Lys Ala Thr Thr Ser Lys Leu Ile
 115 120 125
 Lys Phe Glu Ala Phe Leu Gln Asn Ile
 130 135

(2) INFORMATION FOR SEQ ID NO: 41:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1462 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 41:

GACTTTTAAC AATAAACTA TTGAAGAGTT GCACAATCTC CTTGTCTCTA AGGAAATTTT 60
 TGCAACAGAA TTGACCCAAG CAACACTTGA AAATATCAAG TCTCGTGAGG AAGCCCTCAA 120
 TTCATTTGTC ACCATCGCTG AGGAGCAAGC TCTTGTTCAA GCTAAAGCCA TTGATGAAGC 180
 tGGAATTGAT GCTGACAATG TCCTTTCAGG AATTCCACTT GCTGTTAAGG ATAACATCTC 240
 TACAGACGGT ATTCTCACAA CTGCTGCCTC AAAAATGCTC TACAACTATG AGCCAATCTT 300
 TGATGCGACa gCTgTTGCCA ATGCAAAAAC CAAGGGCATG ATTGTCGTTG GAAAGACCAA 360
 CATGGACGAA TTTGCTATGG GTGGTTCAGG tGAAACTTCA CACTACGGAG CAACTAAAAA 420
 CGCTTGAAC CACAGCAAGG TTCCTGGTGG GTCATCAAGT GGTCTGCCG CAGCTGTAGC 480

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CTCAGGACAA GTTCGCTTGT CACTTGGTTC TGATACTGGT GGTTCATCC GCCAACCTGC 540
 TGCCTTCAAC GGAATCGTTG GTCTCAAACC AACCTACGGA ACAGTTTCAQ GTTTCGGTCT 600
 CATTGCCTTT GGTAGTCAT TAGACCAGAT TGGACCTTTT GCTCCTACTG TTAAGGAAAA 660
 TGCCCTCTTG CTCAACGCTA TTGCCAGCGA AGATGCTAAA GACTCTACTT CTGCTCCTGT 720
 CCGCATCGCC GACTTTACTT CAAAAATCGG CCAAGACATC AAGGGTATGA AAATCGCTTT 780
 GCCTAAGGAA TACCTAGGCG AAGGAATTGA TCCAGAGGTT AAGGAAACAA TCTTAAACGC 840
 GGCCAAACAC TTTGAAAAAT TGGGTGCTAT CGTCGAAGAA GTCAGCCTTC CTCACTCTAA 900
 ATACGGTGTT GCCGTTTATT ACATCATCGC TTCATCAGAA GCTTCATCAA ACTTGCAACG 960
 CTTCGACGGT ATCCGTTACG GCTATCGCGC AGAAGATGCA ACCAACCTTG ATGAAATCTA 1020
 TGTAACAGC CGAAGCCAAG GTTTTGGTGA AGAGGTAAAA CGTCGTATCA TGCTGGGTAC 1080
 TTTCAGTCTT TCATCAGGTT ACTATGATGC CTAATAAAA AAGGCTGGTC AAGTCCGTAC 1140
 CCTCATCATT CAAGATTTTCG AAAAAGTCTT CGCGGATTAC GATTTGATTT TGGGTCCAAC 1200
 TGCTCCAAGT GTTGCCTATG ACTTGGATTC TCTCAACCAT GACCCAGTTG CCATGTACTT 1260
 AGCCGACCTA TTGACCATAC CTGTAAACTT GGCAGGACTG CCTGGAATTT CGATTCTCTG 1320
 TGGATTCTCT CAAGGTCTAC CTGTGGACT CCAATTGATT GGTCCCAAGT ACTCTGAGGA 1380
 AACCATTTAC CAAGCTGCTG CTGCTTTTGA AGCAACAACA GACTACCACA AACAACAACC 1440
 CGTGATTTTT GGAGGTGACA AC 1462

(2) INFORMATION FOR SEQ ID NO:42:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 487 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:42:

Thr Phe Asn Asn Lys Thr Ile Glu Glu Leu His Asn Leu Leu Val Ser
 1 5 10 15

Lys Glu Ile Ser Ala Thr Glu Leu Thr Gln Ala Thr Leu Glu Asn Ile
 20 25 30

Lys Ser Arg Glu Glu Ala Leu Asn Ser Phe Val Thr Ile Ala Glu Glu
 35 40 45

Gln Ala Leu Val Gln Ala Lys Ala Ile Asp Glu Ala Gly Ile Asp Ala
 50 55 60

Asp Asn Val Leu Ser Gly Ile Pro Leu Ala Val Lys Asp Asn Ile Ser
 65 70 75 80

Thr Asp Gly Ile Leu Thr Thr Ala Ala Ser Lys Met Leu Tyr Asn Tyr
 85 90 95
 Glu Pro Ile Phe Asp Ala Thr Ala Val Ala Asn Ala Lys Thr Lys Gly
 100 105 110
 Met Ile Val Val Gly Lys Thr Asn Met Asp Glu Phe Ala Met Gly Gly
 115 120 125
 Ser Gly Glu Thr Ser His Tyr Gly Ala Thr Lys Asn Ala Trp Asn His
 130 135 140
 Ser Lys Val Pro Gly Gly Ser Ser Ser Gly Ser Ala Ala Ala Val Ala
 145 150 155 160
 Ser Gly Gln Val Arg Leu Ser Leu Gly Ser Asp Thr Gly Gly Ser Ile
 165 170 175
 Arg Gln Pro Ala Ala Phe Asn Gly Ile Val Gly Leu Lys Pro Thr Tyr
 180 185 190
 Gly Thr Val Ser Arg Phe Gly Leu Ile Ala Phe Gly Ser Ser Leu Asp
 195 200 205
 Gln Ile Gly Pro Phe Ala Pro Thr Val Lys Glu Asn Ala Leu Leu Leu
 210 215 220
 Asn Ala Ile Ala Ser Glu Asp Ala Lys Asp Ser Thr Ser Ala Pro Val
 225 230 235 240
 Arg Ile Ala Asp Phe Thr Ser Lys Ile Gly Gln Asp Ile Lys Gly Met
 245 250 255
 Lys Ile Ala Leu Pro Lys Glu Tyr Leu Gly Glu Gly Ile Asp Pro Glu
 260 265 270
 Val Lys Glu Thr Ile Leu Asn Ala Ala Lys His Phe Glu Lys Leu Gly
 275 280 285
 Ala Ile Val Glu Glu Val Ser Leu Pro His Ser Lys Tyr Gly Val Ala
 290 295 300
 Val Tyr Tyr Ile Ile Ala Ser Ser Glu Ala Ser Ser Asn Leu Gln Arg
 305 310 315 320
 Phe Asp Gly Ile Arg Tyr Gly Tyr Arg Ala Glu Asp Ala Thr Asn Leu
 325 330 335
 Asp Glu Ile Tyr Val Asn Ser Arg Ser Gln Gly Phe Gly Glu Glu Val
 340 345 350
 Lys Arg Arg Ile Met Leu Gly Thr Phe Ser Leu Ser Ser Gly Tyr Tyr
 355 360 365
 Asp Ala Tyr Tyr Lys Lys Ala Gly Gln Val Arg Thr Leu Ile Ile Gln
 370 375 380
 Asp Phe Glu Lys Val Phe Ala Asp Tyr Asp Leu Ile Leu Gly Pro Thr
 385 390 395 400
 Ala Pro Ser Val Ala Tyr Asp Leu Asp Ser Leu Asn His Asp Pro Val
 405 410 415

0076527 1 012204
 402210 1259260

Ala Met Tyr Leu Ala Asp Leu Leu Thr Ile Pro Val Asn Leu Ala Gly
 420 425 430

Leu Pro Gly Ile Ser Ile Pro Ala Gly Phe Ser Gln Gly Leu Pro Val
 435 440 445

Gly Leu Gln Leu Ile Gly Pro Lys Tyr Ser Glu Glu Thr Ile Tyr Gln
 450 455 460

Ala Ala Ala Ala Phe Glu Ala Thr Thr Asp Tyr His Lys Gln Gln Pro
 465 470 475 480

Val Ile Phe Gly Gly Asp Asn
 485

(2) INFORMATION FOR SEQ ID NO: 43:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 433 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 43:

CTTTACAGGT AAACAAC TAC AAGTCGGCGA CAAGGCGCTT GATTTTTCTC TTACTACAAC 60

AGATCTTTCT AAAAAATCTC TGGCTGATTT TGATGGCAAG AAAAAAGTCT TGAGTGTCGT 120

TCCTTCTATC GATACAGGCA TCTGCTCAAC TCAAACACGT CGTTTTAATG AAGAATTGGC 180

TGGACTGGAC AACACGGTCG TATTGACTGT TTCAATGGAC CTACCTTTTG CTCAAAAACG 240

TTGGTGCGGT GCTGAAGGCC TTGACAATGC CATTATGCTT TCAGACTACT TTGACCATTC 300

TTTCGGGCGC GATTATGCCC TCTTGATCAA CGAATGGCAC CTATTAGCAC GCGCAGTCTT 360

TGTCCTCGAT ACTGACAATA CGATTGCTA CGTTGAATAC GTGGATAATA TCAATTCTGA 420

GCCAAACTTC GAA 433

(2) INFORMATION FOR SEQ ID NO:44:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 144 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:44:

Phe Thr Gly Lys Gln Leu Gln Val Gly Asp Lys Ala Leu Asp Phe Ser
 1 5 10 15

Leu Thr Thr Thr Asp Leu Ser Lys Lys Ser Leu Ala Asp Phe Asp Gly
 20 25 30

Lys Lys Lys Val Leu Ser Val Val Pro Ser Ile Asp Thr Gly Ile Cys

35

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45

Ser Thr Gln Thr Arg Arg Phe Asn Glu Glu Leu Ala Gly Leu Asp Asn
 50 55 60

Thr Val Val Leu Thr Val Ser Met Asp Leu Pro Phe Ala Gln Lys Arg
 65 70 75 80

Trp Cys Gly Ala Glu Gly Leu Asp Asn Ala Ile Met Leu Ser Asp Tyr
 85 90 95

Phe Asp His Ser Phe Gly Arg Asp Tyr Ala Leu Leu Ile Asn Glu Trp
 100 105 110

His Leu Leu Ala Arg Ala Val Phe Val Leu Asp Thr Asp Asn Thr Ile
 115 120 125

Arg Tyr Val Glu Tyr Val Asp Asn Ile Asn Ser Glu Pro Asn Phe Glu
 130 135 140

(2) INFORMATION FOR SEQ ID NO: 45:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 724 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 45:

CCAGGCTGAT ACAAGTATCG CAGACATTCA AAAAAGAGGC GAACTGGTTG TCGGTGTCAA 60

ACAAGACGTT CCCAATTTTG GTTACAAnGA TCCAAGACC GGTACTTATT CTGGTATCGA 120

AaCCGACTTG GCCAAGATGG TAGCTGATGA ACTCAAGGTC AAGATTCGCT ATGTGCCGGT 180

TACAGCACAA ACCCGCGGCC CCCTTCTAGA CAATGAACAG GTCGATATGG ATATCGCGAC 240

CTTTACCATC ACGGACGAAC GCAAAAAACT CTACAACTTT ACCAGTCCCT ACTACACAGA 300

CGCTTCTGGA TTTTGGTCA ATAAATCTGC CAAATCAAA AAGATTGAGG ACCTAAACGG 360

CAAAACCATC GGAGTCGCCC AAGGTTCTAT CACCCAACGC CTGATTACTG AACTGGGTAA 420

AAAGAAAGGT CTGAAGTTTA AATTCGTGCGA ACTTGTTCC TACCCAGAAT TGATTACTTC 480

CCTGCACGCT CATCGTATCG ATACCTTTTC CGTTGACCGC TCTATTCTAT CTGGCTACAC 540

TAGTAAACGG ACAGCACTAC TAGATGATAG TTTCAAGCCA TCTGACTACG GTATTGTTAC 600

CAAGAAATCA AATACAGAGC TCAACGACTA TCTTGATAAC TTGGTTACTA AATGGAGCAA 660

GGATGGTAGT TTGCAGAAAC TTTATGACCG TTACAAGCTC AAACCATCTA GCCATACTGC 720

AGAT 724

(2) INFORMATION FOR SEQ ID NO:46:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 241 amino acids
- (B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:46:

Gln Ala Asp Thr Ser Ile Ala Asp Ile Gln Lys Arg Gly Glu Leu Val
 1 5 10 15
 Val Gly Val Lys Gln Asp Val Pro Asn Phe Gly Tyr Xaa Asp Pro Lys
 20 25 30
 Thr Gly Thr Tyr Ser Gly Ile Glu Thr Asp Leu Ala Lys Met Val Ala
 35 40 45
 Asp Glu Leu Lys Val Lys Ile Arg Tyr Val Pro Val Thr Ala Gln Thr
 50 55 60
 Arg Gly Pro Leu Leu Asp Asn Glu Gln Val Asp Met Asp Ile Ala Thr
 65 70 75 80
 Phe Thr Ile Thr Asp Glu Arg Lys Lys Leu Tyr Asn Phe Thr Ser Pro
 85 90 95
 Tyr Tyr Thr Asp Ala Ser Gly Phe Leu Val Asn Lys Ser Ala Lys Ile
 100 105 110
 Lys Lys Ile Glu Asp Leu Asn Gly Lys Thr Ile Gly Val Ala Gln Gly
 115 120 125
 Ser Ile Thr Gln Arg Leu Ile Thr Glu Leu Gly Lys Lys Lys Gly Leu
 130 135 140
 Lys Phe Lys Phe Val Glu Leu Gly Ser Tyr Pro Glu Leu Ile Thr Ser
 145 150 155 160
 Leu His Ala His Arg Ile Asp Thr Phe Ser Val Asp Arg Ser Ile Leu
 165 170 175
 Ser Gly Tyr Thr Ser Lys Arg Thr Ala Leu Leu Asp Asp Ser Phe Lys
 180 185 190
 Pro Ser Asp Tyr Gly Ile Val Thr Lys Lys Ser Asn Thr Glu Leu Asn
 195 200 205
 Asp Tyr Leu Asp Asn Leu Val Thr Lys Trp Ser Lys Asp Gly Ser Leu
 210 215 220
 Gln Lys Leu Tyr Asp Arg Tyr Lys Leu Lys Pro Ser Ser His Thr Ala
 225 230 235 240
 Asp

(2) INFORMATION FOR SEQ ID NO: 47:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1279 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 47:

GTCTGTATCA TTTGAAAACA AAGAAACAAA CCGTGGTGTG TtgACTTTTCA CTATCTCTCA 60
 AGACCAAATC AAACCAGAAT TGGACCGTGT CTTCAAGtCA GTGAAGAAAT CTCTTAATGT 120
 TCCAGGTTTC CGTAAAGGTC ACCTTCCACG CCCTATCTTC GACCAAAAAT TTGGTGAAGA 180
 AGCTCTTTAT CAAGATGCAA TGAACGCACT TTTGCCAAAC GCTTATGAAG CAGCTGTAAA 240
 AGAAGCTGGT CTTGAAGTGG TTGCCCAACC AAAAATTGAC GTAAC'TTCAA TGGAAAAAGG 300
 TCAAGACTGG GTTATCACTG CTGAAGTCGT TACAAAACCT GAAGTAAAAT TGGGTGACTA 360
 CAAAAACCTT GAAGTATCAG TTGATGTAGA AAAAGAAGTA ACTGACGCTG ATGTCGAAGA 420
 GCGTATCGAA CGCGAACGCA ACAACCTGGC TGAATTGGTT ATCAAGGAAG CTGCTGCTGA 480
 AAACGGCGAC ACTGTTGTGA TCGACTTCGT TGGTTCATC GACGGTGTG AATTTGACGG 540
 TGGAAAAGGT GAAAACTTCT CACTTGGACT TGGTTCAGGT CAATTCATCC CTGGTTTCGA 600
 AGACCAATTG GTAGGTCAC TAGCTGGCGA AACCGTTGAT GTTATCGTAA CATTCCCAGA 660
 AGACTACCAA GCAGAAGACC TTGCAGGTAA AGAAGCTAAA TTCGTGACAA CTATCCACGA 720
 AGTAAAAGCT AAAGAAGTTC CGGCTCTTGA CGATGAACTT GCAAAAGACA TTGATGAAGA 780
 AGTTGAAACA CTTGCTGACT TGAAAGAAAA ATACAGCAAA GAATTGGCTG CTGCTAAAGA 840
 AGAAGCTTAC AAAGATGCAG TTGAAGGTGC AGCAATTGAT ACAGCTGTAG AAAATGCTGA 900
 AATCGTAGAA CTTCCAGAAG AAATGATCCA TGAAGAAGTT CACCGTTCAG TAAATGAATT 960
 CCTTGGGAAT TTGCAACGTC AAGGGATCAA CCCTGACATG TACTTCCAAA TCACTGGAAC 1020
 TACTCAAGAA GACCTTCACA ACCAATACCA AGCAGAAGCT GAGTCACGTA CTAAGACTAA 1080
 CCTTGTATC GAAGCAGTTG CCAAAGCTGA AGGATTTGAT GCTTCAGAAG AAGAAATCCA 1140
 AAAAGAAGTT GAGCAATTGG CAGCAGACTA CAACATGGAA GTTGCACAAG TTCAAAACTT 1200
 GCTTTCAGCT GACATGTTGA AACATGATAT CACTATCAAA AAAGCTGTTG AATTGATCAC 1260
 AAGCACAGCA ACAGTAAAA 1279

(2) INFORMATION FOR SEQ ID NO:48:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 426 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:48:

Ser Val Ser Phe Glu Asn Lys Glu Thr Asn Arg Gly Val Leu Thr Phe

	1				5					10							15
Thr	Ile	Ser	Gln	Asp	Gln	Ile	Lys	Pro	Glu	Leu	Asp	Arg	Val	Phe	Lys		
			20					25					30				
Ser	Val	Lys	Lys	Ser	Leu	Asn	Val	Pro	Gly	Phe	Arg	Lys	Gly	His	Leu		
		35					40					45					
Pro	Arg	Pro	Ile	Phe	Asp	Gln	Lys	Phe	Gly	Glu	Glu	Ala	Leu	Tyr	Gln		
	50					55						60					
Asp	Ala	Met	Asn	Ala	Leu	Leu	Pro	Asn	Ala	Tyr	Glu	Ala	Ala	Val	Lys		
65					70					75					80		
Glu	Ala	Gly	Leu	Glu	Val	Val	Ala	Gln	Pro	Lys	Ile	Asp	Val	Thr	Ser		
				85					90					95			
Met	Glu	Lys	Gly	Gln	Asp	Trp	Val	Ile	Thr	Ala	Glu	Val	Val	Thr	Lys		
			100					105						110			
Pro	Glu	Val	Lys	Leu	Gly	Asp	Tyr	Lys	Asn	Leu	Glu	Val	Ser	Val	Asp		
		115					120					125					
Val	Glu	Lys	Glu	Val	Thr	Asp	Ala	Asp	Val	Glu	Glu	Arg	Ile	Glu	Arg		
	130					135						140					
Glu	Arg	Asn	Asn	Leu	Ala	Glu	Leu	Val	Ile	Lys	Glu	Ala	Ala	Ala	Glu		
145					150					155					160		
Asn	Gly	Asp	Thr	Val	Val	Ile	Asp	Phe	Val	Gly	Ser	Ile	Asp	Gly	Val		
				165				170						175			
Glu	Phe	Asp	Gly	Gly	Lys	Gly	Glu	Asn	Phe	Ser	Leu	Gly	Leu	Gly	Ser		
			180					185					190				
Gly	Gln	Phe	Ile	Pro	Gly	Phe	Glu	Asp	Gln	Leu	Val	Gly	His	Ser	Ala		
		195					200					205					
Gly	Glu	Thr	Val	Asp	Val	Ile	Val	Thr	Phe	Pro	Glu	Asp	Tyr	Gln	Ala		
	210					215					220						
Glu	Asp	Leu	Ala	Gly	Lys	Glu	Ala	Lys	Phe	Val	Thr	Thr	Ile	His	Glu		
225					230					235					240		
Val	Lys	Ala	Lys	Glu	Val	Pro	Ala	Leu	Asp	Asp	Glu	Leu	Ala	Lys	Asp		
				245					250					255			
Ile	Asp	Glu	Glu	Val	Glu	Thr	Leu	Ala	Asp	Leu	Lys	Glu	Lys	Tyr	Ser		
			260					265					270				
Lys	Glu	Leu	Ala	Ala	Ala	Lys	Glu	Glu	Ala	Tyr	Lys	Asp	Ala	Val	Glu		
		275					280					285					
Gly	Ala	Ala	Ile	Asp	Thr	Ala	Val	Glu	Asn	Ala	Glu	Ile	Val	Glu	Leu		
						295					300						
Pro	Glu	Glu	Met	Ile	His	Glu	Glu	Val	His	Arg	Ser	Val	Asn	Glu	Phe		
305					310					315					320		
Leu	Gly	Asn	Leu	Gln	Arg												

159

340

345

350

Ala Glu Ser Arg Thr Lys Thr Asn Leu Val Ile Glu Ala Val Ala Lys
355 360 365

Ala Glu Gly Phe Asp Ala Ser Glu Glu Glu Ile Gln Lys Glu Val Glu
370 375 380

Gln Leu Ala Ala Asp Tyr Asn Met Glu Val Ala Gln Val Gln Asn Leu
385 390 395 400

Leu Ser Ala Asp Met Leu Lys His Asp Ile Thr Ile Lys Lys Ala Val
405 410 415

Glu Leu Ile Thr Ser Thr Ala Thr Val Lys
420 425

(2) INFORMATION FOR SEQ ID NO: 49:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 490 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 49:

TGGTCAAAAG GAAAGTCAGA CAGGAAAGGG GATGAAAATT GTGACCAGTT TTTATCCTAT	60
CTACGCTATG GTTAAGGAAG TATCTGGTGA CTTGAATGAT GTTCGGATGA TTCAGTCAAG	120
TAGTGGTATT CACTCCTTTG AACCTTCGGC AAATGATATC GCAGCCATCT ATGATGCAGA	180
TGTCTTTGTT TACCATTCTC ATACACTCGA ATCTTGGGCA GGAAGTCTGG ATCCAAATCT	240
AAAAAATCC AAAGTGAAGG TCTTAGAGGC TTCTGAGGGA ATGACCTTGG AACGTGTCCC	300
TGGACTAGAG GATGTGGAAG CAGGGGATGG AGTTGATGAA AAAACGCTCT ATGACCCTCA	360
CACATGGCTA GATCCTGAAA AAGCTGGAGA AGAAGCCCAA ATTATCGCTG ATAAACTTTC	420
AGAGGTGGAT AGTGAGCATA AAGAGACTTA TCAAAAAAAT GCGCAACCTT TATCAAAAAA	480
GCTCAGGAAT	490

(2) INFORMATION FOR SEQ ID NO:50:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 163 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:50:

Gly Gln Lys Glu Ser Gln Thr Gly Lys Gly Met Lys Ile Val Thr Ser
1 5 10 15

T02210-1-2339260

160

Phe Tyr Pro Ile Tyr Ala Met Val Lys Glu Val Ser Gly Asp Leu Asn
20 25 30

Asp Val Arg Met Ile Gln Ser Ser Ser Gly Ile His Ser Phe Glu Pro
35 40 45

Ser Ala Asn Asp Ile Ala Ala Ile Tyr Asp Ala Asp Val Phe Val Tyr
50 55 60

His Ser His Thr Leu Glu Ser Trp Ala Gly Ser Leu Asp Pro Asn Leu
65 70 75 80

Lys Lys Ser Lys Val Lys Val Leu Glu Ala Ser Glu Gly Met Thr Leu
85 90 95

Glu Arg Val Pro Gly Leu Glu Asp Val Glu Ala Gly Asp Gly Val Asp
100 105 110

Glu Lys Thr Leu Tyr Asp Pro His Thr Trp Leu Asp Pro Glu Lys Ala
115 120 125

Gly Glu Glu Ala Gln Ile Ile Ala Asp Lys Leu Ser Glu Val Asp Ser
130 135 140

Glu His Lys Glu Thr Tyr Gln Lys Asn Ala Gln Pro Leu Ser Lys Lys
145 150 155 160

Leu Arg Asn

(2) INFORMATION FOR SEQ ID NO: 51:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1006 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 51:

GAAGGATAGA TATATTTTAG CATTTGAGAC ATCCTGTGAT GAGACCAGTG TCGCCGTCTT	60
GAAAAACGAC GATGAGCTCT TGTCCAATGT CATTGCTAGT CAAATTGAGA GTCACAAACG	120
TTTTGGTGCC GTAGTGCCCG AAGTAGCCAG TCGTCACCAT GTCGAGGTCA TTACAGCCTG	180
TATCGAGGAG GCATTGGCAG AAGCAGGGAT TACCGAAGAG GACGTGACAG CTGTTGCGGT	240
TACCTACGGA CCAGGCTTGG TCGGAGCCTT GCTAGTTGGT TTGTCAGCTG CCAAGGCCTT	300
TGCTTGGGCT CACGGACTTC CACTGATTCC TGTTAATCAC ATGGCTGGGC ACCTCATGGC	360
AGCTCAGAGT GTGGAGCCTT TGGAGTTTCC CTTGCTAGCC CTCTTGGTCA GCGGCGGACA	420
CACAGAGTTG GTTTATGTTT CGGAGGCAGG AGATTATAAG ATTGTTGGGG AAACCCGTGA	480
TGATGCGGTT GGTGAGGCTT ATGATAAGGT CGGCCGTGTC ATGGGCTTGA CCTATCCTGC	540
AGGTCGTGAG ATTGACGAGC TGGCTCATCA GGGCAGGAT ATTTATGATT TCCCCCGTGC	600
CATGATTAAG GAAGATAATC TGGAGTTCTC CTTCTCAGGT TTGAAATCTG CCTTTATCAA	660

TCTTCATCAC AATGCCGAGC AAAAGGGAGA AAGCCTGTCT ACAGAAGATT TGTGTGCTTC 720
 CTTCCAAGCA GCAGTTATGG ACATTCTCAT GGCAAAAACC AAGAAGGCTT TGGAGAAATA 780
 TCCTGTAAAA ATCCTAGTTG TGGCAGGTGG TGTGGCAGCC AATAAAGGTC TCAGAGAACG 840
 CCTAGCAGCC GAAATCACAG ATGTCAAGGT TATCATCCCC CCTCTGCGAC TCTGCGGAGA 900
 CAATGCAGGT ATGATTGCCT ATGCCAGCGT CAGCNAGTGG AACAAAGAAA ACTTCGCAGG 960
 CTGGGACCTC AATGCCAAAC CAAGTCTTGC CTTTGATAACC ATGGAA 1006

(2) INFORMATION FOR SEQ ID NO:52:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 335 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:52:

Lys Asp Arg Tyr Ile Leu Ala Phe Glu Thr Ser Cys Asp Glu Thr Ser
 1 5 10 15
 Val Ala Val Leu Lys Asn Asp Asp Glu Leu Leu Ser Asn Val Ile Ala
 20 25 30
 Ser Gln Ile Glu Ser His Lys Arg Phe Gly Gly Val Val Pro Glu Val
 35 40 45
 Ala Ser Arg His His Val Glu Val Ile Thr Ala Cys Ile Glu Glu Ala
 50 55 60
 Leu Ala Glu Ala Gly Ile Thr Glu Glu Asp Val Thr Ala Val Ala Val
 65 70 75 80
 Thr Tyr Gly Pro Gly Leu Val Gly Ala Leu Leu Val Gly Leu Ser Ala
 85 90 95
 Ala Lys Ala Phe Ala Trp Ala His Gly Leu Pro Leu Ile Pro Val Asn
 100 105 110
 His Met Ala Gly His Leu Met Ala Ala Gln Ser Val Glu Pro Leu Glu
 115 120 125
 Phe Pro Leu Leu Ala Leu Leu Val Ser Gly Gly His Thr Glu Leu Val
 130 135 140
 Tyr Val Ser Glu Ala Gly Asp Tyr Lys Ile Val Gly Glu Thr Arg Asp
 145 150 155 160
 Asp Ala Val Gly Glu Ala Tyr Asp Lys Val Gly Arg Val Met Gly Leu
 165 170 175
 Thr Tyr Pro Ala Gly Arg Glu Ile Asp Glu Leu Ala His Gln Gly Gln
 180 185 190
 Asp Ile Tyr Asp Phe Pro Arg Ala Met Ile Lys Glu Asp Asn Leu Glu

195	200	205
Phe Ser Phe Ser Gly Leu Lys Ser Ala Phe Ile Asn Leu His His Asn		
210	215	220
Ala Glu Gln Lys Gly Glu Ser Leu Ser Thr Glu Asp Leu Cys Ala Ser		
225	230	235 240
Phe Gln Ala Ala Val Met Asp Ile Leu Met Ala Lys Thr Lys Lys Ala		
	245	250 255
Leu Glu Lys Tyr Pro Val Lys Ile Leu Val Val Ala Gly Gly Val Ala		
	260	265 270
Ala Asn Lys Gly Leu Arg Glu Arg Leu Ala Ala Glu Ile Thr Asp Val		
	275	280 285
Lys Val Ile Ile Pro Pro Leu Arg Leu Cys Gly Asp Asn Ala Gly Met		
	290	295 300
Ile Ala Tyr Ala Ser Val Ser Xaa Trp Asn Lys Glu Asn Phe Ala Gly		
305	310	315 320
Trp Asp Leu Asn Ala Lys Pro Ser Leu Ala Phe Asp Thr Met Glu		
	325	330 335

(2) INFORMATION FOR SEQ ID NO: 53:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1000 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 53:

GGTAGTTAAA GTTGGTATTA ACGGTTTCGG ACGTATCGGT CGTCTTGCTT TCCGTCGTAT	60
CCAAAACGTA GAAGGTGTTG AAGTTACACG CATCAACGAC CTTACAGATC CAGTTATGCT	120
TGCACACTTG TTGAAATACG ACACAACCTCA AGGTCGTTTC GACGGTACTG TTGAAGTTAA	180
AGAAGGTGGA TTTGAAGTTA ACGGTAAATT CATCAAAGTT TCTGCTGAAC GTGATCCAGA	240
ACAAATCGAC TGGGCTACTG ACGGTGTAGA AATCGTTCTT GAAGCTACTG GTTTCTTTGC	300
TAAGAAAGAA GCAGCTGAAA AACACCTTAA AGGTGGAGCT AAAAAAGTTG TTATCACTGC	360
TCCTGGTGGA AACGACGTTA AAACAGTTGT ATTCAACACT AACCACGACG TTCTTGACGG	420
TACTGAAACA GTTATCTCAG GTGCTTCATG TACTACAAAC TGCTTGCTC CAATGGCTAA	480
AGCTCTTCAA GACAACCTTG GTGTTGTTGA AGGATTGATG ACTACTATCC ACGCTTACAC	540
TGGTGACCAA ATGATCCTTG ACGGACCACA CCGTGGTGGT GACCTTCGCC GTGCTCGCGC	600
TGGTGCTGCA AACATCGTTC CTAACCTAAC TGGTGCTGCA AAAGCTATCG GTCTTGTAAT	660
CCCAGAATTG AATGGTAAAC TTGACGGATC TGCACAACGC GTTCCAACCTC CAACTGGATC	720
AGTTACTGAA TTGGTAGCAG TTCTTGAAAA GAACGTTACT GTTGATGAAG TGAACGCAGC	780

TATGAAAGCA GCTTCAAACG AATCATACGG TTACACAGAA GATCCAATCG TATCTTCAGA 840
 TATCGTAGGT ATGTCTTACG GTTCATTGTT TGACGCAACT CAAACTAAAG TTCTTGACGT 900
 TGACGGTAAA CAATTGGTTA AAGTTGTATC ATGGTACGAC AACGAAATGT CATACTACTGC 960
 ACAACTTGTT CGTACTCTTG GAATACTTCG CAAAAATTGC 1000

(2) INFORMATION FOR SEQ ID NO:54:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 333 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:54:

Val Val Lys Val Gly Ile Asn Gly Phe Gly Arg Ile Gly Arg Leu Ala
 1 5 10 15
 Phe Arg Arg Ile Gln Asn Val Glu Gly Val Glu Val Thr Arg Ile Asn
 20 25 30
 Asp Leu Thr Asp Pro Val Met Leu Ala His Leu Leu Lys Tyr Asp Thr
 35 40 45
 Thr Gln Gly Arg Phe Asp Gly Thr Val Glu Val Lys Glu Gly Gly Phe
 50 55 60
 Glu Val Asn Gly Lys Phe Ile Lys Val Ser Ala Glu Arg Asp Pro Glu
 65 70 75 80
 Gln Ile Asp Trp Ala Thr Asp Gly Val Glu Ile Val Leu Glu Ala Thr
 85 90 95
 Gly Phe Phe Ala Lys Lys Glu Ala Ala Glu Lys His Leu Lys Gly Gly
 100 105 110
 Ala Lys Lys Val Val Ile Thr Ala Pro Gly Gly Asn Asp Val Lys Thr
 115 120 125
 Val Val Phe Asn Thr Asn His Asp Val Leu Asp Gly Thr Glu Thr Val
 130 135 140
 Ile Ser Gly Ala Ser Cys Thr Thr Asn Cys Leu Ala Pro Met Ala Lys
 145 150 155 160
 Ala Leu Gln Asp Asn Phe Gly Val Val Glu Gly Leu Met Thr Thr Ile
 165 170 175
 His Ala Tyr Thr Gly Asp Gln Met Ile Leu Asp Gly Pro His Arg Gly
 180 185 190
 Gly Asp Leu Arg Arg Ala Arg Ala Gly Ala Ala Asn Ile Val Pro Asn
 195 200 205
 Ser Thr Gly Ala Ala Lys Ala Ile Gly Leu Val Ile Pro Glu Leu Asn
 210 215 220

Gly Lys Leu Asp Gly Ser Ala Gln Arg Val Pro Thr Pro Thr Gly Ser
 225 230 235 240
 Val Thr Glu Leu Val Ala Val Leu Glu Lys Asn Val Thr Val Asp Glu
 245 250 255
 Val Asn Ala Ala Met Lys Ala Ala Ser Asn Glu Ser Tyr Gly Tyr Thr
 260 265 270
 Glu Asp Pro Ile Val Ser Ser Asp Ile Val Gly Met Ser Tyr Gly Ser
 275 280 285
 Leu Phe Asp Ala Thr Gln Thr Lys Val Leu Asp Val Asp Gly Lys Gln
 290 295 300
 Leu Val Lys Val Val Ser Trp Tyr Asp Asn Glu Met Ser Tyr Thr Ala
 305 310 315 320
 Gln Leu Val Arg Thr Leu Gly Ile Leu Arg Lys Asn Cys
 325 330

(2) INFORMATION FOR SEQ ID NO: 55:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2389 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 55:

TTCTTACGAG TTGGGACTGT ATCAAGCTAG AACGGTTAAG GAAAATAATC GTGTTTCCTA	60
TATAGATGGA AAACAAGCGA CGCAAAAAC GGAGAATTTG ACTCCTGATG AGGTTAGCAA	120
GCGTGAAGGA ATCAATGCTG AGCAAATCGT CATCAAGATA ACAGACCAAG GCTATGTCAC	180
TTCACATGGC GACCACTATC ATTATTACAA TGGTAAGGTT CCTTATGACG CTATCATCAG	240
TGAAGAATTA CTCATGAAAG ATCCAAACTA TAAGCTAAAA GATGAGGATA TTGTTAATGA	300
GGTCAAGGGT GGATATGTTA TCAAGGTAGA TGGAAAATAC TATGTTTACC TTAAGGATGC	360
TGCCCACGCG GATAACGTCC GTACAAAAGA GGAAATCAAT CGACAAAAC AAGAGCATAG	420
TCAACATCGT GAAGGTGGAA CTCCAAGAAA CGATGGTGCT GTTGCCCTGG CACGTTTCGCA	480
AGGACGCTAT ACTACAGATG ATGGTTATAT CTTTAATGCT TCTGATATCA TAGAGGATAC	540
TGGTGATGCT TATATCGTTC CTCATGGAGA TCATTACCAT TACATTCCTA AGAATGAGTT	600
ATCAGCTAGC GAGTTGGCTG CTGCAGAAGC CTTCTATCT GGTGAGGAA ATCTGTCAAA	660
TTCAAGAACC TATCGCCGAC AAAATAGCGA TAACACTTCA AGAACAAACT GGGTACCTTC	720
TGTAAGCAAT CCAGGAATA CAAATACTAA CACAAGCAAC AACAGCAACA CTAACAGTCA	780
AGCAAGTCAA AGTAATGACA TTGATAGTCT CTTGAAACAG CTCTACAAAC TGCCTTTGAG	840
TCAACGACAT GTAGAATCTG ATGGCCTTGT CTTTGATCCA GCACAAATCA CAAGTCGAAC	900
AGCTAGAGGT GTTGCACTGC CACACGGAGA TCATTACCAC TTCATCCCTT ACTCTCAAT	960

GTCTGAATTG GAAGAACGAA TCGCTCGTAT TATTCCCCTT CGTTATCGTT CAAACCATTG 1020
 GGTACCAGAT TCAAGGCCAG AACAACCAAG TCCACAACCG ACTCCGGAAC CTAGTCCAGG 1080
 CCCGCAACCT GCACCAAATC TTAAATAGA CTCAAATTCT TCTTTGGTTA GTCAGCTGGT 1140
 ACGAAAAGTT GGGGAAGGAT ATGTATTCTGA AGAAAAGGGC ATCTCTCGTT ATGTCTTTGC 1200
 GAAAGATTTA CCATCTGAAA CTGTTAAAAA TCTTGAAAGC AAGTTATCAA AACAAGAGAG 1260
 TGTTCACAC ACTTTAACTG CTAAAAAGA AAATGTTGCT CCTCGTGACC AAGAATTTTA 1320
 TGATAAAGCA TATAATCTGT TAACTGAGGC TCATAAAGCC TTGTTTGNA AATAAGGGTCG 1380
 TAATTCTGAT TTCCAAGCCT TAGACAAATT ATTAGAACGC TTGAATGATG AATCGACTAA 1440
 TAAAGAAAAA TTGGTAGATG ATTTATTGGC ATTCCTAGCA CCAATTACCC ATCCAGAGCG 1500
 ACTTGGCAAA CCAAATTCTC AAATTGAGTA TACTGAAGAC GAAGTTCGTA TTGCTCAATT 1560
 AGCTGATAAG TATACAACGT CAGATGGTTA CATTTTTGAT GAACATGATA TAATCAGTGA 1620
 TGAAGGAGAT GCATATGTAA CGCCTCATAT GGGCCATAGT CACTGGATTG GAAAAGATAG 1680
 CCTTTCTGAT AAGGAAAAAG TTGCAGCTCA AGCCTATACT AAAGAAAAAG GTATCCTACC 1740
 TCCATCTCCA GACGCAGATG TTAAAGCAAA TCCAAGTGA GATAGTGCAG CAGCTATTTA 1800
 CAATCGTGTG AAAGGGGAAA AACGAATTCC ACTCGTTCGA CTTCCATATA TGGTTGAGCA 1860
 TACAGTTGAG GTTAAAAACG GTAATTTGAT TATTCCTCAT AAGGATCATT ACCATAATAT 1920
 TAAATTTGCT TGGTTTGATG ATCACACATA CAAAGCTCCA AATGGCTATA CCTTGGAAGA 1980
 TTTGTTTGCG ACGATTAAGT ACTACGTAGA ACACCCTGAC GAACGTCCAC ATTCTAATGA 2040
 TGGATGGGGC AATGCCAGTG AGCATGTGTT AGGCAAGAAA GACCACAGTG AAGATCCAAA 2100
 TAAGAACTTC AAAGCGGATG AAGAGCCAGT AGAGGAAACA CCTGCTGAGC CAGAAGTCCC 2160
 TCAAGTAGAG ACTGAAAAAG TAGAAGCCCA ACTCAAAGAA GCAGAAGTTT TGCTTGCGAA 2220
 AGTAACGGAT TCTAGTCTGA AAGCCAATGC AACAGAACT CTAGCTGGTT TACGAAATAA 2280
 TTTGACTCTT CAAATTATGG ATAACAATAG TATCATGGCA GAAGCAGAAA AATTACTTGC 2340
 GTTGTTAAAA GGAAGTAATC CTTATCTGT AAGTAAGGAA AAAATAAAC 2389

(2) INFORMATION FOR SEQ ID NO:56:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 796 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:56:

Ser Tyr Glu Leu Gly Leu Tyr Gln Ala Arg Thr Val Lys Glu Asn Asn

1	5	10	15
Arg Val Ser Tyr	Ile Asp Gly Lys	Gln Ala Thr Gln	Lys Thr Glu Asn
20	25	30	
Leu Thr Pro Asp	Glu Val Ser Lys	Arg Glu Gly Ile	Asn Ala Glu Gln
35	40	45	
Ile Val Ile Lys	Ile Thr Asp Gln	Gly Tyr Val Thr	Ser His Gly Asp
50	55	60	
His Tyr His Tyr	Tyr Asn Gly Lys	Val Pro Tyr Asp	Ala Ile Ile Ser
65	70	75	80
Glu Glu Leu Leu	Met Lys Asp Pro	Asn Tyr Lys Leu	Lys Asp Glu Asp
85	90	95	
Ile Val Asn Glu	Val Lys Gly Gly	Tyr Val Ile Lys	Val Asp Gly Lys
100	105	110	
Tyr Tyr Val Tyr	Leu Lys Asp Ala	Ala His Ala Asp	Asn Val Arg Thr
115	120	125	
Lys Glu Glu Ile	Asn Arg Gln Lys	Gln Glu His Ser	Gln His Arg Glu
130	135	140	
Gly Gly Thr Pro	Arg Asn Asp Gly	Ala Val Ala Leu	Ala Arg Ser Gln
145	150	155	160
Gly Arg Tyr Thr	Thr Asp Asp Gly	Tyr Ile Phe Asn	Ala Ser Asp Ile
165	170	175	
Ile Glu Asp Thr	Gly Asp Ala Tyr	Ile Val Pro His	Gly Asp His Tyr
180	185	190	
His Tyr Ile Pro	Lys Asn Glu Leu	Ser Ala Ser Glu	Leu Ala Ala Ala
195	200	205	
Glu Ala Phe Leu	Ser Gly Arg Gly	Asn Leu Ser Asn	Ser Arg Thr Tyr
210	215	220	
Arg Arg Gln Asn	Ser Asp Asn Thr	Ser Arg Thr Asn	Trp Val Pro Ser
225	230	235	240
Val Ser Asn Pro	Gly Thr Thr Asn	Thr Asn Thr Ser	Asn Asn Ser Asn
245	250	255	
Thr Asn Ser Gln	Ala Ser Gln Ser	Asn Asp Ile Asp	Ser Leu Leu Lys
260	265	270	
Gln Leu Tyr Lys	Leu Pro Leu Ser	Gln Arg His Val	Glu Ser Asp Gly
275	280	285	
Leu Val Phe Asp	Pro Ala Gln Ile	Thr Ser Arg Thr	Ala Arg Gly Val
290	295	300	
Ala Val Pro His	Gly Asp His Tyr	His Phe Ile Pro	Tyr Ser Gln Met
305	310	315	320
Ser Glu Leu Glu	Glu Arg Ile Ala	Arg Ile Ile Pro	Leu Arg Tyr Arg
325	330	335	
Ser Asn His Trp	Val Pro Asp Ser	Arg Pro Glu Gln	Pro Ser Pro Gln

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10220-225200

167

340

345

350

Pro Thr Pro Glu Pro Ser Pro Gly Pro Gln Pro Ala Pro Asn Leu Lys
355 360 365

Ile Asp Ser Asn Ser Ser Leu Val Ser Gln Leu Val Arg Lys Val Gly
370 375 380

Glu Gly Tyr Val Phe Glu Glu Lys Gly Ile Ser Arg Tyr Val Phe Ala
385 390 395 400

Lys Asp Leu Pro Ser Glu Thr Val Lys Asn Leu Glu Ser Lys Leu Ser
405 410 415

Lys Gln Glu Ser Val Ser His Thr Leu Thr Ala Lys Lys Glu Asn Val
420 425 430

Ala Pro Arg Asp Gln Glu Phe Tyr Asp Lys Ala Tyr Asn Leu Leu Thr
435 440 445

Glu Ala His Lys Ala Leu Phe Xaa Asn Lys Gly Arg Asn Ser Asp Phe
450 455 460

Gln Ala Leu Asp Lys Leu Leu Glu Arg Leu Asn Asp Glu Ser Thr Asn
465 470 475 480

Lys Glu Lys Leu Val Asp Asp Leu Leu Ala Phe Leu Ala Pro Ile Thr
485 490 495

His Pro Glu Arg Leu Gly Lys Pro Asn Ser Gln Ile Glu Tyr Thr Glu
500 505 510

Asp Glu Val Arg Ile Ala Gln Leu Ala Asp Lys Tyr Thr Thr Ser Asp
515 520 525

Gly Tyr Ile Phe Asp Glu His Asp Ile Ile Ser Asp Glu Gly Asp Ala
530 535 540

Tyr Val Thr Pro His Met Gly His Ser His Trp Ile Gly Lys Asp Ser
545 550 555 560

Leu Ser Asp Lys Glu Lys Val Ala Ala Gln Ala Tyr Thr Lys Glu Lys
565 570 575

Gly Ile Leu Pro Pro Ser Pro Asp Ala Asp Val Lys Ala Asn Pro Thr
580 585 590

Gly Asp Ser Ala Ala Ala Ile Tyr Asn Arg Val Lys Gly Glu Lys Arg
595 600 605

Ile Pro Leu Val Arg Leu Pro Tyr Met Val Glu His Thr Val Glu Val
610 615 620

Lys Asn Gly Asn Leu Ile Ile Pro His Lys Asp His Tyr His Asn Ile
625 630 635 640

Lys Phe Ala Trp Phe Asp Asp His Thr Tyr Lys Ala Pro Asn Gly Tyr
645 650 655

—Thr—Leu—Glu—Asp—Leu Phe Ala Thr Ile Lys Tyr Tyr Val Glu His Pro
660 665 670

Asp Glu Arg Pro His Ser Asn Asp Gly Trp Gly Asn Ala Ser Glu His

00765274 043004
T000T0 T255260

(2) INFORMATION FOR SEQ ID NO: 57:

(A) LENGTH: 1180 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

TACTGAGATG	CATCATAATC	TAGGAGCTGA	AAAGCGTTCA	GCATGGGCTA	CTACTATCGA	60
TAGTTTTTAAG	GAGCGAAGTC	AAAAAGTCAG	AGCACTATCT	GATCCAAATG	TGCGTTTTGT	120
TCCCTTCTTT	GGCTCTAGTG	AATGGCTTCG	TTTTGACGGT	GCTCATTCTG	CGGTATTAGC	180
TGAGAAATAC	AATCGTTCCT	ACCGTCCTTA	TCTTTTAGGA	CAGGGGGGAG	CTGCATCGCT	240
TAACCAATAT	TTTGGAATGC	AACAGATGTT	ACCACAGCTG	GAGAATAAAC	AAGTTGTGTA	300
TGTTATCTCA	CCTCAGTGGT	TCAGTAAAAA	TGGCTATGAT	CCAGCAGCCT	TCCAGCAGTA	360
TTTTAATGGA	GACCAGTTGA	CTAGTTTTCT	GAAACATCAA	TCTGGGGATC	AGGCTAGTCA	420
ATATGCAGCG	ACTCGCTTAC	TGCAACAGTT	CCCAAACGTA	GCTATGAAGG	ACCTGGTTCA	480
GAAGTTGGCA	AGTAAAGAAG	AATTGTCGAC	AGCAGACAAT	GAAATGATTG	AATTATTGGC	540
TCGTTTTAAT	GAACGCCAAG	CTTCCTTTTT	TGGTCAGTTT	TCGGTTAGAG	GCTATGTTAA	600
CTACGATAAG	CATGTAGCTA	AGTATTTAAA	AATCTTGCCA	GACCACTTTT	CTTATCAGGC	660
AATAGAAGAT	GTTGTCAAAG	CAGATGCTGA	AAAAAATACT	TCCAATAATG	AGATGGGAAT	720
GGAAAATTAT	TTCTATAATG	AGCAGATCAA	GAAGGATTTG	AAGAAATTAA	AGGATTCTCA	780
GAAAAGCTTT	ACCTATCTCA	AGTCGCCAGA	GTATAATGNN	TTGCAGTTGG	TTTTAACACA	840

GTTTTCTAAA TCTAAGGTAA ACCCGATTTT TATCATTTCCA CCTGTTAATA AAAAATGGAT 900
 GNACTATGCT GGTCTACGAG AGGATATGTA CCAACAAACG GTGCAGAAGA TTCGCTACCA 960
 GTTAGAAAGT CAAGGTTTTA CCAATATAGC AGATTTTTTCT AAGGACGGCG GGGAGCCTTT 1020
 CTTTATGAAG GACACCATT CACCTTGTTG GTTGGGTTGG TTGGCTTTTG ACAAGGCAGT 1080
 TGATCCTTTC CTATCCAATC CCACACCAGC TCCGACTTAC CATCTGAATG AGCGCTTTTT 1140
 CAGCAAAGAT TGGGCGACTT ATGATGGAGA TGTCAAAGAA 1180

(2) INFORMATION FOR SEQ ID NO:58:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 393 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:58:

Thr	Glu	Met	His	His	Asn	Leu	Gly	Ala	Glu	Lys	Arg	Ser	Ala	Val	Ala	1	5	10	15
Thr	Thr	Ile	Asp	Ser	Phe	Lys	Glu	Arg	Ser	Gln	Lys	Val	Arg	Ala	Leu	20	25	30	
Ser	Asp	Pro	Asn	Val	Arg	Phe	Val	Pro	Phe	Phe	Gly	Ser	Ser	Glu	Trp	35	40	45	
Leu	Arg	Phe	Asp	Gly	Ala	His	Ser	Ala	Val	Leu	Ala	Glu	Lys	Tyr	Asn	50	55	60	
Arg	Ser	Tyr	Arg	Pro	Tyr	Leu	Leu	Gly	Gln	Gly	Gly	Ala	Ala	Ser	Leu	65	70	75	80
Asn	Gln	Tyr	Phe	Gly	Met	Gln	Gln	Met	Leu	Pro	Gln	Leu	Glu	Asn	Lys	85	90	95	
Gln	Val	Val	Tyr	Val	Ile	Ser	Pro	Gln	Trp	Phe	Ser	Lys	Asn	Gly	Tyr	100	105	110	
Asp	Pro	Ala	Ala	Phe	Gln	Gln	Tyr	Phe	Asn	Gly	Asp	Gln	Leu	Thr	Ser	115	120	125	
Phe	Leu	Lys	His	Gln	Ser	Gly	Asp	Gln	Ala	Ser	Gln	Tyr	Ala	Ala	Thr	130	135	140	
Arg	Leu	Leu	Gln	Gln	Phe	Pro	Asn	Val	Ala	Met	Lys	Asp	Leu	Val	Gln	145	150	155	160
Lys	Leu	Ala	Ser	Lys	Glu	Glu	Leu	Ser	Thr	Ala	Asp	Asn	Glu	Met	Ile	165	170	175	
Glu	Leu	Leu	Ala	Arg	Phe	Asn	Glu	Arg	Gln	Ala	Ser	Phe	Phe	Gly	Gln	180	185	190	
Phe	Ser	Val	Arg	Gly	Tyr	Val	Asn	Tyr	Asp	Lys	His	Val	Ala	Lys	Tyr	195	200	205	

Leu Lys Ile Leu Pro Asp Gln Phe Ser Tyr Gln Ala Ile Glu Asp Val
 210 215 220
 Val Lys Ala Asp Ala Glu Lys Asn Thr Ser Asn Asn Glu Met Gly Met
 225 230 235 240
 Glu Asn Tyr Phe Tyr Asn Glu Gln Ile Lys Lys Asp Leu Lys Lys Leu
 245 250 255
 Lys Asp Ser Gln Lys Ser Phe Thr Tyr Leu Lys Ser Pro Glu Tyr Asn
 260 265 270
 Xaa Leu Gln Leu Val Leu Thr Gln Phe Ser Lys Ser Lys Val Asn Pro
 275 280 285
 Ile Phe Ile Ile Pro Pro Val Asn Lys Lys Trp Met Xaa Tyr Ala Gly
 290 295 300
 Leu Arg Glu Asp Met Tyr Gln Gln Thr Val Gln Lys Ile Arg Tyr Gln
 305 310 315 320
 Leu Glu Ser Gln Gly Phe Thr Asn Ile Ala Asp Phe Ser Lys Asp Gly
 325 330 335
 Gly Glu Pro Phe Phe Met Lys Asp Thr Ile His Leu Gly Trp Leu Gly
 340 345 350
 Trp Leu Ala Phe Asp Lys Ala Val Asp Pro Phe Leu Ser Asn Pro Thr
 355 360 365
 Pro Ala Pro Thr Tyr His Leu Asn Glu Arg Phe Phe Ser Lys Asp Trp
 370 375 380
 Ala Thr Tyr Asp Gly Asp Val Lys Glu
 385 390

(2) INFORMATION FOR SEQ ID NO: 59:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1423 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 59:

GGTTTTGAGA AAGTATTTGC AGGGGGCCCT GATTGAGTCG ATTGAGCAAG TGGAAAATGA	60
CCGTATTGTG GAAATTACAG TTTCCAATAA AAACGAGATT GGAGACCATA TCCAGGCTAC	120
CTTGATTATC GAAATTATGG GGAAACACAG TAATATTCTA CTGGTCGATA AAAGCAGTCA	180
TAAAATCCTC GAAGTTATCA AACACGTCGG CTTTTCACAA AATAGCTACC GCACCTTACT	240
TCCAGGATCG ACCTATATCG CTCCGCCAAG TACAAAATCT CTCAATCCTT TTAATATCAA	300
GGATGAAAAG CTCTTTGAAA TCCTGCAAAC CCAAGAACTA ACAGCAAAAA ATCTTCAAAG	360
CCTCTTTCAA GGTCTGGGAC GCGATACGGC AAATGAATTG GAAAGGATAC TGGTTAGTGA	420

AAAACTTTCC GCTTTCCGAA ATTTTTCCTCA TCAAGAAACC AAGCCATGCT TGA CTGAGAC 480
 TTCCTTCAGT CCAGTTCCTT TTGCAAATCA GGTGGGAGAG CCTTTTGCAA ATCTTTCTGA 540
 TTTGTTGGAC ACCTACTATA AGGATAAGGC TGAGCGCGAC CGCGTCAAAC AGCAGGCCAG 600
 TGA ACTGATT CGTCGTGTTG AAAATGAACT TCAGAAAAAC CGACACAAAC TCAAAAAACA 660
 GGAAAAAGAG TTACTGGCGA CAGACAACGC TGAAGAATTT CGTCAAAAAG GAGAATTGCT 720
 GACAACCTTC CTCCACCAAG TGCCTAACGA CCAAGACCAG GTTATCCTAG ACAACTACTA 780
 TACCAACCAA CCTATCATGA TTGCGCTTGA TAAGGCTCTG ACTCCCAACC AGAATGCCCA 840
 ACGCTATTTT AAACGGTATC AGAAACTCAA AGAAGCTGTC AAATACTTGA CTGATTTGAT 900
 TGAAGAAACC AAAGCCACTA TTCTCTATCT GGAAAGTGTA GAAACCGTCC TCAACCAAGC 960
 TGGACTGGAA GAAATCGCTG AAATCCGTGA AGAATTGATT CAAACAGGTT TTATCCGCAG 1020
 AAGACAACGG GAGAAAATCC AGAAACGCAA AAAACTAGAA CAATATCTAG CAAGCGATGG 1080
 CAAAACCATC ATCTATGTCG GACGAAACAA TCTTCAAAT GAGGAATTGA CCTTTAAAT 1140
 GGCCCGCAAG GAGGAAC TTT GGTTCATGC TAAGGACATT CCTGGAAGCC ATGTTGTCAT 1200
 CTCAGGAAAT CTTGACCCAT CTGATGCAGT CAAGACAGAC GCAGCAGAGT TAGCTGCCTA 1260
 CTTCTCTCAA GGGCGCCTGT CGAATCTGGT GCAGGTAGAT ATGATTGAAG TCAAAAAACT 1320
 CAATAAACCA ACTGGTGGAA AACCCGGCTT TGTCACCTAC ACAGGACAAA AGACCCTCCG 1380
 CGTCACACCA GACTCCAAAA AAATTGCATC CATGAAAAAA TCC 1423

(2) INFORMATION FOR SEQ ID NO:60:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 474 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:60:

Val Leu Arg Lys Tyr Leu Gln Gly Ala Leu Ile Glu Ser Ile Glu Gln
 1 5 10 15

Val Glu Asn Asp Arg Ile Val Glu Ile Thr Val Ser Asn Lys Asn Glu
 20 25 30

Ile Gly Asp His Ile Gln Ala Thr Leu Ile Ile Glu Ile Met Gly Lys
 35 40 45

His Ser Asn Ile Leu Leu Val Asp Lys Ser Ser His Lys Ile Leu Glu
 50 55 60

Val Ile Lys His Val Gly Phe Ser Gln Asn Ser Tyr Arg Thr Leu Leu
 65 70 75 80

Pro Gly Ser Thr Tyr Ile Ala Pro Pro Ser Thr Lys Ser Leu Asn Pro

95

Phe	Thr	Ile	Lys	Asp	Glu	Leu	Glu	Phe	Glu	Ile	Leu	Gln	Thr	Gln	Glu
			100						105					110	
Leu	Thr	Ala	Lys	Asn	Leu	Gln	Ser	Leu	Phe	Gln	Gly	Leu	Gly	Arg	Asp
		115					120					125			
Thr	Ala	Asn	Glu	Leu	Glu	Arg	Ile	Leu	Val	Ser	Glu	Lys	Leu	Ser	Ala
	130					135					140				
Phe	Arg	Asn	Phe	Phe	Asn	Gln	Glu	Thr	Lys	Pro	Cys	Leu	Thr	Glu	Thr
145					150					155					160
Ser	Phe	Ser	Pro	Val	Pro	Phe	Ala	Asn	Gln	Val	Gly	Glu	Pro	Phe	Ala
				165					170					175	
Asn	Leu	Ser	Asp	Leu	Leu	Asp	Thr	Tyr	Tyr	Lys	Asp	Lys	Ala	Glu	Arg
			180					185					190		
Asp	Arg	Val	Lys	Gln	Gln	Ala	Ser	Glu	Leu	Ile	Arg	Arg	Val	Glu	Asn
		195					200					205			
Glu	Leu	Gln	Lys	Asn	Arg	His	Lys	Leu	Lys	Lys	Gln	Glu	Lys	Glu	Leu
	210					215					220				
Leu	Ala	Thr	Asp	Asn	Ala	Glu	Glu	Phe	Arg	Gln	Lys	Gly	Glu	Leu	Leu
225					230					235					240
Thr	Thr	Phe	Leu	His	Gln	Val	Pro	Asn	Asp	Gln	Asp	Gln	Val	Ile	Leu
				245					250					255	
Asp	Asn	Tyr	Tyr	Thr	Asn	Gln	Pro	Ile	Met	Ile	Ala	Leu	Asp	Lys	Ala
			260					265					270		
Leu	Thr	Pro	Asn	Gln	Asn	Ala	Gln	Arg	Tyr	Phe	Lys	Arg	Tyr	Gln	Lys
		275					280					285			
Leu	Lys	Glu	Ala	Val	Lys	Tyr	Leu	Thr	Asp	Leu	Ile	Glu	Glu	Thr	Lys
	290					295					300				
Ala	Thr	Ile	Leu	Tyr	Leu	Glu	Ser	Val	Glu	Thr	Val	Leu	Asn	Gln	Ala
305					310					315					320
Gly	Leu	Glu	Glu	Ile	Ala	Glu	Ile	Arg	Glu	Glu	Leu	Ile	Gln	Thr	Gly
				325					330					335	
Phe	Ile	Arg	Arg	Arg	Gln	Arg	Glu	Lys	Ile	Gln	Lys	Arg	Lys	Lys	Leu
			340					345					350		
Glu	Gln	Tyr	Leu	Ala	Ser	Asp	Gly	Lys	Thr	Ile	Ile	Tyr	Val	Gly	Arg
		355					360					365			
Asn	Asn	Leu	Gln	Asn	Glu	Glu	Leu	Thr	Phe	Lys	Met	Ala	Arg	Lys	Glu
					375						380				
Glu	Leu	Trp	Phe	His	Ala	Lys	Asp	Ile	Pro	Gly	Ser	His	Val	Val	Ile
385					390					395					400
Ser	Gly	Asn	Leu	Asp	Pro	Ser	Asp	Ala	Val	Lys	Thr	Asp	Ala	Ala	Glu
				405					410					415	
Leu	Ala	Ala	Tyr	Phe	Ser	Gln	Gly	Arg	Leu	Ser	Asn	Leu	Val	Gln	Val

173

420

425

430

Asp Met Ile Glu Val Lys Lys Leu Asn Lys Pro Thr Gly Gly Lys Pro
 435 440 445

Gly Phe Val Thr Tyr Thr Gly Gln Lys Thr Leu Arg Val Thr Pro Asp
 450 455 460

Ser Lys Lys Ile Ala Ser Met Lys Lys Ser
 465 470

(2) INFORMATION FOR SEQ ID NO: 61:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 544 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 61:

GACAACATTT ACTATCCATA CAGTAGAGTC AGCACCAGCA GAAGTGAAAG AAATTCTTGA 60
 AACAGTAGAA AAAGACAACA ATGGCTATAT TCCCAACCTA ATCGGTCTCT TGGCCAATGC 120
 CCCGACTGTT TTAGAAGCCT ACCAAATTGT CTCATCTATC CACCGTCGCA ACAGCCTGAC 180
 ACCCGTTGAG CGTGAAGTGG TGCAAATCAC GGCAGCCGTG ACCAATGGTT GTGCCTTCTG 240
 TGTCGCAGGT CACACAGCCT TTTCCATCAA ACAAATCCAG ATGAATGATG ACTTGATTCA 300
 AGCTCTTCGC AATCGTACTC CAATTGAAAC AGATCCTAAA TTGGATACCC TAGCTAAGTT 360
 TACCTTGGCA GTTATCAATA CCAAGGGTCG TGTAGGAGAT GAAGCCTTGT CTGAGTTTTT 420
 AGAAGCTGGC TACACTCAAC AAAATGCCTT GGATGTGGTT TTTGGTGTCA GCCTAGCAAT 480
 CCTCTGTAAC TATGCCAACA ACTTAGCTAA TACACCAATT AATCCAGAAT TGCAACCTTA 540
 TGCC 544

(2) INFORMATION FOR SEQ ID NO:62:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 181 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:62:

Thr Thr Phe Thr Ile His Thr Val Glu Ser Ala Pro Ala Glu Val Lys
 1 5 10 15

Glu Ile Leu Glu Thr Val Glu Lys Asp Asn Asn Gly Tyr Ile Pro Asn
 20 25 30

Leu Ile Gly Leu Leu Ala Asn Ala Pro Thr Val Leu Glu Ala Tyr Gln

35										40										45										
Ile	Val	Ser	Ser	Ile	His	Arg	Arg	Asn	Ser	Leu	Thr	Pro	Val	Glu	Arg															
50								55						60																
Glu	Val	Val	Gln	Ile	Thr	Ala	Ala	Val	Thr	Asn	Gly	Cys	Ala	Phe	Cys															
65					70					75				80																
Val	Ala	Gly	His	Thr	Ala	Phe	Ser	Ile	Lys	Gln	Ile	Gln	Met	Asn	Asp															
				85					90					95																
Asp	Leu	Ile	Gln	Ala	Leu	Arg	Asn	Arg	Thr	Pro	Ile	Glu	Thr	Asp	Pro															
			100					105					110																	
Lys	Leu	Asp	Thr	Leu	Ala	Lys	Phe	Thr	Leu	Ala	Val	Ile	Asn	Thr	Lys															
		115					120					125																		
Gly	Arg	Val	Gly	Asp	Glu	Ala	Leu	Ser	Glu	Phe	Leu	Glu	Ala	Gly	Tyr															
	130					135					140																			
Thr	Gln	Gln	Asn	Ala	Leu	Asp	Val	Val	Phe	Gly	Val	Ser	Leu	Ala	Ile															
145					150					155					160															
Leu	Cys	Asn	Tyr	Ala	Asn	Asn	Leu	Ala	Asn	Thr	Pro	Ile	Asn	Pro	Glu															
				165					170					175																
Leu	Gln	Pro	Tyr	Ala																										
				180																										

(2) INFORMATION FOR SEQ ID NO: 63:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 811 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 63:

GGCTAAGGAA AGAGTGGATG TACTAGCTTA TAAACAGGGG TTGTTTGAAA CGAGAGAGCA	60
GGCCAAGCGA GGTGTGATGG CTGGCCTAGT CGTAGCAGTC CTTAATGGAG AACGGTTTGA	120
CAAGCCAGGA GAGAAAATTC CAGATGACAC CGAATTAAAA CTCAAGGGGG AGAAACTCAA	180
GTATGTCAGC CGTGGTGGTT TGAAACTGGA AAAGGCCTTG CAGGTCTTTG ATTTGTCGGT	240
GGATGGCGCG ACTACGATTG ATATCGGGGC CTCTACTGGA GGTTTTACCG ATGTCATGCT	300
ACAGAATAGT GCCAAGTTGG TCTTTGCAGT CGATGTTGGT ACCAATCAGT TGGCTTGGA	360
ATTACGCCAA GACCCACGAG TTGTCAGCAT GGAGCAGTTC AATTTCGCT ATGCTGAAAA	420
GACTGATTTC GAGCAGGAGC CGAGCTTTGC CAGTATTGAT GTGAGTTTCA TTTCCCTTAG	480
TCTGATTTTG CCAGCCTTGC ACCGTGTCTT GGCTGATCAA GGTCAGGTGG TAGCACTTGT	540
CAAACCTCAG TTTGAGGCAG GACGTGAGCA GATTGGGAAA AATGGAATTA TTCGAGATGC	600
TAAGGTTTCAT CAGAATGTCC TTGAATCTGT AACAGCTATG GCAGTAGAGG TAGGTTTTTC	660

AGTCCTTGGC TTGGACTTTT CTCCCATCCA AGGTGGACAT GGAAATATTG AATTTTTCAGC 720
 GTATTTGAAA AAAGAAAAGT CAGCAAGCAA TCAGATTCTT GCTGAGATTA AAGAAGCAGT 780
 AGAGAGGGCG CATAGTCAAT TAAAAATGA A 811

(2) INFORMATION FOR SEQ ID NO:64:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 270 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:64:

Ala Lys Glu Arg Val Asp Val Leu Ala Tyr Lys Gln Gly Leu Phe Glu
 1 5 10 15
 Thr Arg Glu Gln Ala Lys Arg Gly Val Met Ala Gly Leu Val Val Ala
 20 25 30
 Val Leu Asn Gly Glu Arg Phe Asp Lys Pro Gly Glu Lys Ile Pro Asp
 35 40 45
 Asp Thr Glu Leu Lys Leu Lys Gly Glu Lys Leu Lys Tyr Val Ser Arg
 50 55 60
 Gly Gly Leu Lys Leu Glu Lys Ala Leu Gln Val Phe Asp Leu Ser Val
 65 70 75 80
 Asp Gly Ala Thr Thr Ile Asp Ile Gly Ala Ser Thr Gly Gly Phe Thr
 85 90 95
 Asp Val Met Leu Gln Asn Ser Ala Lys Leu Val Phe Ala Val Asp Val
 100 105 110
 Gly Thr Asn Gln Leu Ala Trp Lys Leu Arg Gln Asp Pro Arg Val Val
 115 120 125
 Ser Met Glu Gln Phe Asn Phe Arg Tyr Ala Glu Lys Thr Asp Phe Glu
 130 135 140
 Gln Glu Pro Ser Phe Ala Ser Ile Asp Val Ser Phe Ile Ser Leu Ser
 145 150 155 160
 Leu Ile Leu Pro Ala Leu His Arg Val Leu Ala Asp Gln Gly Gln Val
 165 170 175
 Val Ala Leu Val Lys Pro Gln Phe Glu Ala Gly Arg Glu Gln Ile Gly
 180 185 190
 Lys Asn Gly Ile Ile Arg Asp Ala Lys Val His Gln Asn Val Leu Glu
 195 200 205
 Ser Val Thr Ala Met Ala Val Glu Val Gly Phe Ser Val Leu Gly Leu
 210 215 220
 Asp Phe Ser Pro Ile Gln Gly Gly His Gly Asn Ile Glu Phe Leu Ala
 225 230 235 240

Lys Glu Ala Val Glu Arg Ala His Ser Gln Phe Lys Asn Glu
260 265 270

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2290 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

TTGTTCCCTAT	GAACCTTGGTC	GTCACCAAGC	TGGTCAGGTT	AAGAAAAGAGT	CTAATCGAGT	60
TTCTTATATA	GATGGTGATC	AGGCTGGTCA	AAAGGCAGAA	AACTTGACAC	CAGATGAAGT	120
CAGTAAGAGG	GAGGGGATCA	ACGCCGAACA	AATNGTNATC	AAGATTACGG	ATCAAGGTTA	180
TGTGACCTCT	CATGGAGACC	ATTATCATT	CTATAATGGC	AAGGTTCCCT	ATGATGCCAT	240
CATCAGTGAA	GAGCTCCTCA	TGAAAGATCC	GAATTATCAG	TTGAAGGATT	CAGACATTGT	300
CAATGAAATC	AAGGGTGGTT	ATGTCATTAA	GGTAAACGGT	AAATACTATG	TNTACCTTAA	360
GGATGCAGCT	CATGCGGATA	ATATTCCGGAC	AAAAGAAGAG	ATTAAACGTC	AGAAGCAGGA	420
ACGCAGTCAT	AATCATAACT	CAAGAGCAGA	TAATGCTGTT	GCTGCAGCCA	GAGCCCAAGG	480
ACGTTATACA	ACGGATGATG	GGTATATCTT	CAATGCATCT	GATATCATTG	AGGACACGGG	540
TGATGCTTAT	ATCGTTCCTC	ACGGCGACCA	TTACCATTAC	ATTCCCTAAGA	ATGAGTTATC	600
AGCTAGCGAG	TTAGCTGCTG	CAGAAGCCTA	TTGGAATGGG	AAGCAGGGAT	CTCGTCCTTC	660
TTCAAGTTCT	AGTTATAATG	CAAATCCAGC	TCAACCAAGA	TTGTCAGAGA	ACCACAATCT	720
GA CTG TCACT	CCA ACTTATC	ATCAAAATCA	AGGGGAAAAC	ATTTCAAGCC	TTTTACGTGA	780
ATTGTATGCT	AAACCCTTAT	CAGAACGCCA	TGTGGAATCT	GATGGCCTTA	TTTTCGACCC	840
AGCGCAAATC	ACAAGTCGAA	CCGCCAGAGG	TGTAGCTGTC	CCTCATGGTA	ACCATTACCA	900
CTTTATCCCT	TATGAACAAA	TGTCTGAATT	GGAAAAACGA	ATTGCTCGTA	TTATTCCCTT	960
TCGTTATCGT	TCAAACCATT	GGGTACCAGA	TTCAAGACCA	GAACAACCAA	GTCCACAATC	1020
GA CTCCG GAA	CCTAGTCCAA	GTCCGCAACC	TGCACCAAAT	CCTCAACCAG	CTCCAAGCAA	1080
TCCAATTGAT	GAGAAATTGG	TCAAAGAAGC	TGTTCGAAAA	GTAGGCGATG	GTTATGTCTT	1140
TGAGGAGAAT	GGAGTTTCTC	GTTATATCCC	AGCCAAGGAT	CTTTCAGCAG	AAACAGCAGC	1200
AGGCATTGAT	AGCAAACCTGG	CCAAGCAGGA	AAGTTTATCT	CATAAGCTAG	GAGCTAAGAA	1260
AACTGACCTC	CCATCTAGTG	ATCGAGAATT	TTACAATAAG	GCTTATGACT	TACTAGCAAG	1320

AATTCACCAA GATTACTTG ATAATAAAGG TCGACAAGTT GATTTTGAGG CTTTGGATAA 1380
 CCTGTTGGAA CGACTCAAGG ATGTCNCAAG TGATAAAGTC AAGTTAGTGG ANGATATTCT 1440
 TGCCTTCTTA GCTCCGATTC GTCATCCAGA ACGTTTAGGA AAACCAAATG CGCAAATTAC 1500
 CTACACTGAT GATGAGATTC AAGTAGCCAA GTTGGCAGGC AAGTACACAA CAGAAGACGG 1560
 TTATATCTTT GATCCTCGTG ATATAACCAG TGATGAGGGG GATGCCTATG TAACTCCACA 1620
 TATGACCCAT AGCCACTGGA TTAAAAAGA TAGTTTGTCT GAAGCTGAGA GAGCGGCAGC 1680
 CCAGGCTTAT GCTAAAGAGA AAGGTTTGAC CCCTCCTTCG ACAGACCATC AGGATTTCAGG 1740
 AAATACTGAG GCAAAAGGAG CAGAAGCTAT CTACAACCGC GTGAAAGCAG CTAAGAAGGT 1800
 GCCACTTGAT CGTATGCCTT ACAATCTTCA ATATACTGTA GAAGTCAAAA ACGGTAGTTT 1860
 AATCATACCT CATTATGACC ATTACCATAA CATCAAATTT GAGTGGTTTG ACGAAGGCCT 1920
 TTATGAGGCA CCTAAGGGGT ATACTCTTGA GGATCTTTTG GCGACTGTCA AGTACTATGT 1980
 CGAACATCCA AACGAACGTC CGCATTGAGA TAATGGTTTT GGTAACGCTA GCGACCATGT 2040
 TCAAAGAAAC AAAAATGGTC AAGCTGATAC CAATCAAACG GAAAAACCAA GCGAGGAGAA 2100
 ACCTCAGACA GAAAAACCTG AGGAAGAAAC CCCTCGAGAA GAGAAACCGC AAAGCGAGAA 2160
 ACCAGAGTCT CCAAACCAA CAGAGGAACC AGAAGAATCA CCAGAGGAAT CAGAAGAACC 2220
 TCAGGTCGAG ACTGAAAAGG TTGAAGAAAA ACTGAGAGAG GCTGAAGATT TACTTGAAAA 2280
 AATCCAGGAT 2290

(2) INFORMATION FOR SEQ ID NO:66:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 763 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:66:

Cys Ser Tyr Glu Leu Gly Arg His Gln Ala Gly Gln Val Lys Lys Glu
 1 5 10 15
 Ser Asn Arg Val Ser Tyr Ile Asp Gly Asp Gln Ala Gly Gln Lys Ala
 20 25 30
 Glu Asn Leu Thr Pro Asp Glu Val Ser Lys Arg Glu Gly Ile Asn Ala
 35 40 45
 Glu Gln Xaa Val Ile Lys Ile Thr Asp Gln Gly Tyr Val Thr Ser His
 50 55 60
 Gly Asp His Tyr His Tyr Tyr Asn Gly Lys Val Pro Tyr Asp Ala Ile
 65 70 75 80
 Ile Ser Glu Glu Leu Leu Met Lys Asp Pro Asn Tyr Gln Leu Lys Asp

				85					90					95	
Ser	Asp	Ile	Val	Asn	Glu	Ile	Lys	Gly	Gly	Tyr	Val	Ile	Lys	Val	Asn
			100					105					110		
Gly	Lys	Tyr	Tyr	Val	Tyr	Leu	Lys	Asp	Ala	Ala	His	Ala	Asp	Asn	Ile
		115					120					125			
Arg	Thr	Lys	Glu	Glu	Ile	Lys	Arg	Gln	Lys	Gln	Glu	Arg	Ser	His	Asn
	130					135					140				
His	Asn	Ser	Arg	Ala	Asp	Asn	Ala	Val	Ala	Ala	Ala	Arg	Ala	Gln	Gly
145					150					155					160
Arg	Tyr	Thr	Thr	Asp	Asp	Gly	Tyr	Ile	Phe	Asn	Ala	Ser	Asp	Ile	Ile
				165					170					175	
Glu	Asp	Thr	Gly	Asp	Ala	Tyr	Ile	Val	Pro	His	Gly	Asp	His	Tyr	His
			180					185					190		
Tyr	Ile	Pro	Lys	Asn	Glu	Leu	Ser	Ala	Ser	Glu	Leu	Ala	Ala	Ala	Glu
		195					200					205			
Ala	Tyr	Trp	Asn	Gly	Lys	Gln	Gly	Ser	Arg	Pro	Ser	Ser	Ser	Ser	Ser
	210					215					220				
Tyr	Asn	Ala	Asn	Pro	Ala	Gln	Pro	Arg	Leu	Ser	Glu	Asn	His	Asn	Leu
225					230					235					240
Thr	Val	Thr	Pro	Thr	Tyr	His	Gln	Asn	Gln	Gly	Glu	Asn	Ile	Ser	Ser
				245					250					255	
Leu	Leu	Arg	Glu	Leu	Tyr	Ala	Lys	Pro	Leu	Ser	Glu	Arg	His	Val	Glu
			260					265					270		
Ser	Asp	Gly	Leu	Ile	Phe	Asp	Pro	Ala	Gln	Ile	Thr	Ser	Arg	Thr	Ala
		275					280					285			
Arg	Gly	Val	Ala	Val	Pro	His	Gly	Asn	His	Tyr	His	Phe	Ile	Pro	Tyr
	290					295					300				
Glu	Gln	Met	Ser	Glu	Leu	Glu	Lys	Arg	Ile	Ala	Arg	Ile	Ile	Pro	Leu
305					310					315					320
Arg	Tyr	Arg	Ser	Asn	His	Trp	Val	Pro	Asp	Ser	Arg	Pro	Glu	Gln	Pro
				325					330					335	
Ser	Pro	Gln	Ser	Thr	Pro	Glu	Pro	Ser	Pro	Ser	Pro	Gln	Pro	Ala	Pro
			340					345					350		
Asn	Pro	Gln	Pro	Ala	Pro	Ser	Asn	Pro	Ile	Asp	Glu	Lys	Leu	Val	Lys
		355					360					365			
Glu	Ala	Val	Arg	Lys	Val	Gly	Asp	Gly	Tyr	Val	Phe	Glu	Glu	Asn	Gly
	370					375					380				
Val	Ser	Arg	Tyr	Ile	Pro	Ala	Lys	Asp	Leu	Ser	Ala	Glu	Thr	Ala	Ala
385					390					395					400
Gly	Ile	Asp	Ser	Lys	Leu	Ala	Lys	Gln	Glu	Ser	Leu	Ser	His	Lys	Leu
				405					410					415	
Gly	Ala	Lys	Lys	Thr	Asp	Leu	Pro	Ser	Ser	Asp	Arg	Glu	Phe	Tyr	Asn

430

Lys	Ala	Tyr	Asp	Leu	Leu	Ala	Arg	Ile	His	Gln	Asp	Leu	Leu	Asp	Asn	---
	435							440					445			
Lys	Gly	Arg	Gln	Val	Asp	Phe	Glu	Ala	Leu	Asp	Asn	Leu	Leu	Glu	Arg	
	450					455					460					
Leu	Lys	Asp	Val	Xaa	Ser	Asp	Lys	Val	Lys	Leu	Val	Xaa	Asp	Ile	Leu	
465					470					475					480	
Ala	Phe	Leu	Ala	Pro	Ile	Arg	His	Pro	Glu	Arg	Leu	Gly	Lys	Pro	Asn	
				485					490					495		
Ala	Gln	Ile	Thr	Tyr	Thr	Asp	Asp	Glu	Ile	Gln	Val	Ala	Lys	Leu	Ala	
			500					505					510			
Gly	Lys	Tyr	Thr	Thr	Glu	Asp	Gly	Tyr	Ile	Phe	Asp	Pro	Arg	Asp	Ile	
		515					520					525				
Thr	Ser	Asp	Glu	Gly	Asp	Ala	Tyr	Val	Thr	Pro	His	Met	Thr	His	Ser	
	530					535					540					
His	Trp	Ile	Lys	Lys	Asp	Ser	Leu	Ser	Glu	Ala	Glu	Arg	Ala	Ala	Ala	
545					550					555					560	
Gln	Ala	Tyr	Ala	Lys	Glu	Lys	Gly	Leu	Thr	Pro	Pro	Ser	Thr	Asp	His	
				565					570					575		
Gln	Asp	Ser	Gly	Asn	Thr	Glu	Ala	Lys	Gly	Ala	Glu	Ala	Ile	Tyr	Asn	
			580					585					590			
Arg	Val	Lys	Ala	Ala	Lys	Lys	Val	Pro	Leu	Asp	Arg	Met	Pro	Tyr	Asn	
		595					600					605				
Leu	Gln	Tyr	Thr	Val	Glu	Val	Lys	Asn	Gly	Ser	Leu	Ile	Ile	Pro	His	
	610					615					620					
Tyr	Asp	His	Tyr	His	Asn	Ile	Lys	Phe	Glu	Trp	Phe	Asp	Glu	Gly	Leu	
625					630				635						640	
Tyr	Glu	Ala	Pro	Lys	Gly	Tyr	Thr	Leu	Glu	Asp	Leu	Leu	Ala	Thr	Val	
				645					650					655		
Lys	Tyr	Tyr	Val	Glu	His	Pro	Asn	Glu	Arg	Pro	His	Ser	Asp	Asn	Gly	
			660					665					670			
Phe	Gly	Asn	Ala	Ser	Asp	His	Val	Gln	Arg	Asn	Lys	Asn	Gly	Gln	Ala	
		675					680					685				
Asp	Thr	Asn	Gln	Thr	Glu	Lys	Pro	Ser	Glu	Glu	Lys	Pro	Gln	Thr	Glu	
	690					695					700					
Lys	Pro	Glu	Glu	Glu	Thr	Pro	Arg	Glu	Glu	Lys	Pro	Gln	Ser	Glu	Lys	
705					710					715					720	
Pro	Glu	Ser	Pro	Lys	Pro	Thr	Glu	Glu	Pro	Glu	Glu	Ser	Pro	Glu	Glu	
				725					730					735		
Ser	Glu	Glu	Pro	Gln	Val	Glu	Thr	Glu	Lys	Val	Glu	Glu	Lys	Leu	Arg	
			740					745					750			
Glu	Ala	Glu	Asp	Leu	Leu	Gly	Lys	Ile	Gln	Asp						

755

760

(2) INFORMATION FOR SEQ ID NO: 67:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 352 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 67:

TTATAAGGGT GAATTAGAAA AAGGATACCA ATTTGATGGT TGGGAAATTT CTGGTTTCGA 60
 AGGTAAAAAA GACGCTGGCT ATGTTATTAA TCTATCAAAA GATACCTTTA TAAACCTGT 120
 ATTCAAGAAA ATAGAGGAGA AAAAGGAGGA AGAAAATAAA CCTACTTTTG ATGTATCGAA 180
 AAAGAAAGAT AACCCACAAG TAAACCATAG TCAATTAAAT GAAAGTCACA GAAAAGAGGA 240
 TTTACAAAGA GAAGAGCATT CACAAAAATC TGATTCAACT AAGGATGTTA CAGCTACAGT 300
 TCTTGATAAA AACAATATCA GTAGTAAATC AACTACTAAC AATCCTAATA AG 352

(2) INFORMATION FOR SEQ ID NO:68:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 117 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:68:

Tyr Lys Gly Glu Leu Glu Lys Gly Tyr Gln Phe Asp Gly Trp Glu Ile
 1 5 10 15
 Ser Gly Phe Glu Gly Lys Lys Asp Ala Gly Tyr Val Ile Asn Leu Ser
 20 25 30
 Lys Asp Thr Phe Ile Lys Pro Val Phe Lys Lys Ile Glu Glu Lys Lys
 35 40 45
 Glu Glu Glu Asn Lys Pro Thr Phe Asp Val Ser Lys Lys Asp Asn
 50 55 60
 Pro Gln Val Asn His Ser Gln Leu Asn Glu Ser His Arg Lys Glu Asp
 65 70 75 80
 Leu Gln Arg Glu Glu His Ser Gln Lys Ser Asp Ser Thr Lys Asp Val
 85 90 95
 Thr Ala Thr Val Leu Asp Lys Asn Asn Ile Ser Ser Lys Ser Thr Thr
 100 105 110
 Asn Asn Pro Asn Lys
 115

(2) INFORMATION FOR SEQ ID NO: 69:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1312 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 69:

GAATGTTTCAG GCTCAAGAAA GTTCAGGAAA TAAATCCAC TTTATCAATG TTCAAGAAGG 60

TGGCAGTGAT GCGATTATTC TTGAAAGCAA TGGACATTTT GCCATGGTGG ATACAGGAGA 120

AGATTATGAT TTCCCAGATG GAAGTGATTC TCGCTATCCA TGGAGAGAAG GAATTGAAAC 180

GTCTTATAAG CATGTTCTAA CAGACCGTGT CTTTCGTCGT TTGAAGGAAT TGGGTGTCCA 240

AAACTTGAT TTTATTTTGG TGACCCATAC CCACAGTGAT CATATTGGAA ATGTTGATGA 300

ATTACTGTCT ACCTATCCAG TTGACCGAGT CTATCTTAAG AAATATAGTG ATAGTCGTAT 360

TACTAATTCT GAACGTCTAT GGGATAATCT GTATGGCTAT GATAAGGTTT TACAGACTGC 420

TGCAGAAAAA GGTGTTTCAG TTATTCAAAA TATCACACAA GGGGATGCTC ATTTTCAGTT 480

TGGGGACATG GATATTCAGC TCTATAATTA TGAAAATGAA ACTGATTCAT CGGGTGAATT 540

AAAGAAAATT TGGGATGACA ATTCCAATTC CTTGATTAGC GTGGTGAAAG TCAATGGCAA 600

GAAAATTTAC CTTGGGGGCG ATTTAGATAA TGTTTCATGGA GCAGAAGACA AGTATGGTCC 660

TCTCATTGGA AAAGTTGATT TGATGAAGTT TAATCATCAC CATGATACCA ACAAATCAAA 720

TACCAAGGAT TTCATTAAAA ATTTGAGTCC GAGTTTGATT GTTCAAACCT CGGATAGTCT 780

ACCTTGAAA AATGGTGTTG ATAGTGAGTA TGTTAATTGG CTCAAAGAAC GAGGAATTGA 840

GAGAATCAAC GCAGCCAGCA AAGACTATGA TGCAACAGTT TTTGATATTC GAAAAGACGG 900

TTTTGTCAAT ATTTCAACAT CCTACAAGCC GATTCCAAGT TTTCAAGCTG GTTGGCATAA 960

GAGTGCATAT GGGAACGGT GGTATCAAGC GCCTGATTCT ACAGGAGAGT ATGCTGTCTGG 1020

TTGGAATGAA ATCGAAGGTG AATGGTATTA CTTTAACCAA ACGGGTATCT TGTTACAGAA 1080

TCAATGGAAG AAATGGAACA ATCATTGGTT CTATTTGACA GACTCTGGTG CTTCTGCTAA 1140

AAATTGGAAG AAAATCGCTG GAATCTGGTA TTATTTTAAC AAAGAAAACC AGATGGAAAT 1200

TGGTTGGATT CAAGATAAAG AGCAGTGGTA TTATTTGGAT GTTGATGGTT CTATGAAGAC 1260

AGGATGGCTT CAATATATGG GGCAATGGTA TTACTTTGCT CCATCAGGGG AA 1312

(2) INFORMATION FOR SEQ ID NO:70:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 437 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

00765274 012204
102210 1225260

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:70:

Asn	Val	Gln	Ala	Gln	Glu	Ser	Ser	Gly	Asn	Lys	Ile	His	Phe	Ile	Asn	
1				5					10					15		
Val	Gln	Glu	Gly	Gly	Ser	Asp	Ala	Ile	Ile	Leu	Glu	Ser	Asn	Gly	His	
			20					25					30			
Phe	Ala	Met	Val	Asp	Thr	Gly	Glu	Asp	Tyr	Asp	Phe	Pro	Asp	Gly	Ser	
		35					40					45				
Asp	Ser	Arg	Tyr	Pro	Trp	Arg	Glu	Gly	Ile	Glu	Thr	Ser	Tyr	Lys	His	
	50					55					60					
Val	Leu	Thr	Asp	Arg	Val	Phe	Arg	Arg	Leu	Lys	Glu	Leu	Gly	Val	Gln	
65					70					75					80	
Lys	Leu	Asp	Phe	Ile	Leu	Val	Thr	His	Thr	His	Ser	Asp	His	Ile	Gly	
				85					90					95		
Asn	Val	Asp	Glu	Leu	Leu	Ser	Thr	Tyr	Pro	Val	Asp	Arg	Val	Tyr	Leu	
			100					105					110			
Lys	Lys	Tyr	Ser	Asp	Ser	Arg	Ile	Thr	Asn	Ser	Glu	Arg	Leu	Trp	Asp	
		115					120					125				
Asn	Leu	Tyr	Gly	Tyr	Asp	Lys	Val	Leu	Gln	Thr	Ala	Ala	Glu	Lys	Gly	
	130					135					140					
Val	Ser	Val	Ile	Gln	Asn	Ile	Thr	Gln	Gly	Asp	Ala	His	Phe	Gln	Phe	
145					150					155					160	
Gly	Asp	Met	Asp	Ile	Gln	Leu	Tyr	Asn	Tyr	Glu	Asn	Glu	Thr	Asp	Ser	
				165					170					175		
Ser	Gly	Glu	Leu	Lys	Lys	Ile	Trp	Asp	Asp	Asn	Ser	Asn	Ser	Leu	Ile	
			180					185					190			
Ser	Val	Val	Lys	Val	Asn	Gly	Lys	Lys	Ile	Tyr	Leu	Gly	Gly	Asp	Leu	
		195					200					205				
Asp	Asn	Val	His	Gly	Ala	Glu	Asp	Lys	Tyr	Gly	Pro	Leu	Ile	Gly	Lys	
	210					215					220					
Val	Asp	Leu	Met	Lys	Phe	Asn	His	His	His	Asp	Thr	Asn	Lys	Ser	Asn	
225					230					235					240	
Thr	Lys	Asp	Phe	Ile	Lys	Asn	Leu	Ser	Pro	Ser	Leu	Ile	Val	Gln	Thr	
				245					250					255		
Ser	Asp	Ser	Leu	Pro	Trp	Lys	Asn	Gly	Val	Asp	Ser	Glu	Tyr	Val	Asn	
			260					265					270			
Trp	Leu	Lys	Glu	Arg	Gly	Ile	Glu	Arg	Ile	Asn	Ala	Ala	Ser	Lys	Asp	
		275					280					285				
Tyr	Asp	Ala	Thr	Val	Phe	Asp	Ile	Arg	Lys	Asp	Gly	Phe	Val	Asn	Ile	
	290					295					300					

Ser Thr Ser Tyr Lys Pro Ile Pro Ser Phe Gln Ala Gly Trp His Lys
305 310 315 320

Ser-Ala Tyr Gly Asn Trp Trp Tyr Gln Ala Pro Asp Ser Thr Gly Glu
325 330 335

Tyr Ala Val Gly Trp Asn Glu Ile Glu Gly Glu Trp Tyr Tyr Phe Asn
340 345 350

Gln Thr Gly Ile Leu Leu Gln Asn Gln Trp Lys Lys Trp Asn Asn His
355 360 365

Trp Phe Tyr Leu Thr Asp Ser Gly Ala Ser Ala Lys Asn Trp Lys Lys
370 375 380

Ile Ala Gly Ile Trp Tyr Tyr Phe Asn Lys Glu Asn Gln Met Glu Ile
385 390 395 400

Gly Trp Ile Gln Asp Lys Glu Gln Trp Tyr Tyr Leu Asp Val Asp Gly
405 410 415

Ser Met Lys Thr Gly Trp Leu Gln Tyr Met Gly Gln Trp Tyr Tyr Phe
420 425 430

Ala Pro Ser Gly Glu
435

(2) INFORMATION FOR SEQ ID NO: 71:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1855 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 71:

CTTGGGTGTA ACCCATATCC AGCTCCTTCC AGTCTTGTCT TACTACTTTG TCAATGAATT	60
GAAAAACCAT GAACGCTTGT CTGACTACGC TTCAAGCAAC AGCAACTACA ACTGGGGATA	120
TGACCCTCAA AACTACTTCT CCTTGACTGG TATGTACTCA AGCGATCCTA AGAATCCAGA	180
AAAACGAATC GCAGAATTTA AAAACCTCAT CAACGAAATC CACAAACGTG GTATGGGAGC	240
TATCCTAGAT GTCGTTTATA ACCACACAGC CAAAGTCGAT CTCTTTGAAG ATTTGGAACC	300
AAACTACTAC CACTTTATGG ATGCCGATGG CACACCTCGA ACTAGCTTTG GTGGTGGACG	360
CTTGGGGACA ACCCACCATA TGACCAAACG GCTCCTAATT GACTCTATCA AATACCTAGT	420
TGATACCTAC AAAGTGGATG GCTTCCGTTT CGATATGATG GGAGACCATG ACGCCGCTTC	480
TATCGAAGAA GCTTACAAGG CTGCACGCGC CCTCAATCCA AACCTCATCA TGCTTGGTGA	540
AGGTTGGAGA ACCTATGCCG GTGATGAAAA CATGCCTACT AAAGCTGCTG ACCAAGATTG	600
GATGAAACAT ACCGATACTG TCGCTGTCTT TTCAGATGAC ATCCGTAACA ACCTCAAATC	660
TGGTTATCCA AACGAAGGTC AACCTGCCTT TATCACAGGT GGCAAGCGTG ATGTCAACAC	720

CATCTTTAAA AATCTCATTG CTCAACCAAC TAACTTTGAA GCTGACAGCC CTGGAGATGT 780
 CATCCAATAC ATCGCAGCCC ATGATAACTT GACCCTCTTT GACATCATTG CCCAGTCTAT 840
 CAAAAAAGAC CCAAGCAAGG CTGAGAACTA TGCTGAAATC CACCGTCGTT TACGACTTGG 900
 AAATCTCATG GTCTTGACAG CTCAAGGAAC TCCATTTATC CACTCCGGTC AGGAATATGG 960
 ACGTACTAAA CAATTCCTGT ACCCAGCCTA CAAGACTCCA GTAGCAGAGG ATAAGGTTCC 1020
 AAACAAATCT CACTTGTTGC GTGATAAGGA CGGCAACCCA TTTGACTATC CTTACTTCAT 1080
 CCATGACTCT TACGATTCTA GTGATGCAGT CAACAAGTTT GACTGGACTA AGGCTACAGA 1140
 TGGTAAAGCT TATCCTGAAA ATGTCAAGAG CCGTGACTAT ATGAAAGGTT TGATTGCCCT 1200
 TCGTCAATCT ACAGATGCCT TCCGACTTAA GAGTCTTCAA GATATCAAAG ACCGTGTCCA 1260
 CCTCATCACT GTCCCAGGCC AAAATGGTGT GGAAAAAGAG GATGTAGTGA TTGGCTACCA 1320
 AATCACTGCT CCAAACGGCG ATATCTACGC AGTCTTTGTC AATGCGGATG AAAAAGCTCG 1380
 CGAATTTAAT TTGGGAACTG CCTTTGCACA TCTAAGAAAT GCGGAAGTTT TGGCAGATGA 1440
 AAACCAAGCA GGACCAGTCG GAATTGCCAA CCCGAAAGGA CTTGAATGGA CTGAAAAAGG 1500
 CTTGAAATTG AATGCCCTTA CAGCTACTGT TCTTCGAGTC TCTCAAAATG GAACTAGCCA 1560
 TGAGTCAACT GCAGAAGAGA AACCAGACTC AACCCTTCC AAGCCTGAAC ATCAAAATGA 1620
 AGCTTCTCAC CCTGCACATC AAGACCCAGC TCCAGAAGCT AGACCTGATT CTACTAAACC 1680
 AGATGCCAAA GTAGCTGATG CGGAAAATAA ACCTAGCCAA GCTACAGCTG ATTCACAAGC 1740
 TGAACAACCA GCACAAGAAG CACAAGCATC ATCTGTAAAA GAAGCGGTTC GAAACGAATC 1800
 GGTAGAAAAC TCTAGCAAGG AAAATATACC TGCAACCCCA GATAACAAG CTGAA 1855

(2) INFORMATION FOR SEQ ID NO:72:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 618 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:72:

Leu Gly Val Thr His Ile Gln Leu Leu Pro Val Leu Ser Tyr Tyr Phe
 1 5 10 15
 Val Asn Glu Leu Lys Asn His Glu Arg Leu Ser Asp Tyr Ala Ser Ser
 20 25 30
 Asn Ser Asn Tyr Asn Trp Gly Tyr Asp Pro Gln Asn Tyr Phe Ser Leu
 35 40 45
 Thr Gly Met Tyr Ser Ser Asp Pro Lys Asn Pro Glu Lys Arg Ile Ala
 50 55 60

Glu Phe Lys Asn Leu Ile Asn Glu Ile His Lys Arg Gly Met Gly Ala
 65 70 75 80
 Ile Leu Asp Val Val Tyr Asn His Thr Ala Lys Val Asp Leu Phe Glu
 85 90 95
 Asp Leu Glu Pro Asn Tyr Tyr His Phe Met Asp Ala Asp Gly Thr Pro
 100 105 110
 Arg Thr Ser Phe Gly Gly Gly Arg Leu Gly Thr Thr His His Met Thr
 115 120 125
 Lys Arg Leu Leu Ile Asp Ser Ile Lys Tyr Leu Val Asp Thr Tyr Lys
 130 135 140
 Val Asp Gly Phe Arg Phe Asp Met Met Gly Asp His Asp Ala Ala Ser
 145 150 155 160
 Ile Glu Glu Ala Tyr Lys Ala Ala Arg Ala Leu Asn Pro Asn Leu Ile
 165 170 175
 Met Leu Gly Glu Gly Trp Arg Thr Tyr Ala Gly Asp Glu Asn Met Pro
 180 185 190
 Thr Lys Ala Ala Asp Gln Asp Trp Met Lys His Thr Asp Thr Val Ala
 195 200 205
 Val Phe Ser Asp Asp Ile Arg Asn Asn Leu Lys Ser Gly Tyr Pro Asn
 210 215 220
 Glu Gly Gln Pro Ala Phe Ile Thr Gly Gly Lys Arg Asp Val Asn Thr
 225 230 235 240
 Ile Phe Lys Asn Leu Ile Ala Gln Pro Thr Asn Phe Glu Ala Asp Ser
 245 250 255
 Pro Gly Asp Val Ile Gln Tyr Ile Ala Ala His Asp Asn Leu Thr Leu
 260 265 270
 Phe Asp Ile Ile Ala Gln Ser Ile Lys Lys Asp Pro Ser Lys Ala Glu
 275 280 285
 Asn Tyr Ala Glu Ile His Arg Arg Leu Arg Leu Gly Asn Leu Met Val
 290 295 300
 Leu Thr Ala Gln Gly Thr Pro Phe Ile His Ser Gly Gln Glu Tyr Gly
 305 310 315 320
 Arg Thr Lys Gln Phe Arg Asp Pro Ala Tyr Lys Thr Pro Val Ala Glu
 325 330 335
 Asp Lys Val Pro Asn Lys Ser His Leu Leu Arg Asp Lys Asp Gly Asn
 340 345 350
 Pro Phe Asp Tyr Pro Tyr Phe Ile His Asp Ser Tyr Asp Ser Ser Asp
 355 360 365
 Ala Val Asn Lys Phe Asp Trp Thr Lys Ala Thr Asp Gly Lys Ala Tyr
 370 375 380
 Pro Glu Asn Val Lys Ser Arg Asp Tyr Met Lys Gly Leu Ile Ala Leu
 385 390 395 400

Arg Gln Ser Thr Asp Ala Phe Arg Leu Lys Ser Leu Gln Asp Ile Lys
405 410 415

Asp Arg Val His Leu Ile Thr Val Pro Gly Gln Asn Gly Val Glu Lys
420 425 430

Glu Asp Val Val Ile Gly Tyr Gln Ile Thr Ala Pro Asn Gly Asp Ile
435 440 445

Tyr Ala Val Phe Val Asn Ala Asp Glu Lys Ala Arg Glu Phe Asn Leu
450 455 460

Gly Thr Ala Phe Ala His Leu Arg Asn Ala Glu Val Leu Ala Asp Glu
465 470 475 480

Asn Gln Ala Gly Pro Val Gly Ile Ala Asn Pro Lys Gly Leu Glu Trp
485 490 495

Thr Glu Lys Gly Leu Lys Leu Asn Ala Leu Thr Ala Thr Val Leu Arg
500 505 510

Val Ser Gln Asn Gly Thr Ser His Glu Ser Thr Ala Glu Glu Lys Pro
515 520 525

Asp Ser Thr Pro Ser Lys Pro Glu His Gln Asn Glu Ala Ser His Pro
530 535 540

Ala His Gln Asp Pro Ala Pro Glu Ala Arg Pro Asp Ser Thr Lys Pro
545 550 555 560

Asp Ala Lys Val Ala Asp Ala Glu Asn Lys Pro Ser Gln Ala Thr Ala
565 570 575

Asp Ser Gln Ala Glu Gln Pro Ala Gln Glu Ala Gln Ala Ser Ser Val
580 585 590

Lys Glu Ala Val Arg Asn Glu Ser Val Glu Asn Ser Ser Lys Glu Asn
595 600 605

Ile Pro Ala Thr Pro Asp Lys Gln Ala Glu
610 615

(2) INFORMATION FOR SEQ ID NO: 73:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1774 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 73:

TAGTGATGGT ACTTGGCAAG GAAAACAGTA TCTGAAAGAA GATGGCAGTC AAGCAGCAAA	60
TGAGTGGGTT TTNGATACTC ATTATCAATC TTGGTTCTAT ATAAAAGCAG ATGCTAACTA	120
TGCTGAAAAT GAATGGCTAA AGCAAGGTGA CGACTATTTT TACCTCAAAT CTGGTGGCTA	180
TATGGCCAAA TCAGAATGGG TAGAAGACAA GGGAGCCTTT TATTATCTTG ACCAAGATGG	240
AAAGATGAAA AGAAATGCTT GGGTAGGAAC TTCCTATGTT GGTGCAACAG GTGCCAAAGT	300

AATAGAAGAC TGGGTCTATG ATTCTCAATA CGATGCTTGG TTTTATATCA AAGCAGATGG 360
 ACAGCACGCA GAGAAAGAAT GGCTCCAAAT TAAAGGGAAG GACTATTATT TCAAATCCGG 420
 TGGTTATCTA CTGACAAGTC AGTGGATTAA TCAAGCTTAT GTGAATGCTA GTGGTGCCAA 480
 AGTACAGCAA GGTGCGCTTT TTGACAAACA ATACCAATCT TGGTTTTACA TCAAAGAAAA 540
 TGGAAACTAT GCTGATAAAG AATGGATTTT CGAGAATGGT CACTATTATT ATCTAAAATC 600
 CGGTGGCTAC ATGGCAGCCA ATGAATGGAT TTGGGATAAG GAATCTTGGT TTTATCTCAA 660
 ATTTGATGGG AAAATGGCTG AAAAAGAATG GGTCTACGAT TCTCATAGTC AAGCTTGGA 720
 CTACTTCAAA TCCGGTGGTT ACATGACAGC CAATGAATGG ATTTGGGATA AGGAATCTTG 780
 GTTTTACCTC AAATCTGATG GGAAAATAGC TGAAAAAGAA TGGGTCTACG ATTCTCATAG 840
 TCAAGCTTGG TACTACTTCA AATCTGGTGG CTACATGGCG AAAAATGAGA CAGTAGATGG 900
 TTATCAGCTT GGAAGCGATG GTAAATGGCT TGGAGGAAAA ACTACAAATG AAAATGCTGC 960
 TTACTATCAA GTAGTGCCTG TTACAGCCAA TGTTTATGAT TCAGATGGTG AAAAGCTTTC 1020
 CTATATATCG CAAGGTAGTG TCGTATGGCT AGATAAGGAT AGAAAAAGTG ATGACAAGCG 1080
 CTTGGCTATT ACTATTTCTG GTTTGTCAGG CTATATGAAA ACAGAAGATT TACAAGCGCT 1140
 AGATGCTAGT AAGGACTTTA TCCCTTATTA TGAGAGTGAT GGCCACCGTT TTTATCACTA 1200
 TGTGGCTCAG AATGCTAGTA TCCCAGTAGC TTCTCATCTT TCTGATATGG AAGTAGGCAA 1260
 GAAATATTAT TCGGCAGATG GCCTGCATTT TGATGGTTTT AAGCTTGAGA ATCCCTTCCT 1320
 TTTCAAAGAT TTAACAGAGG CTACAAACTA CAGTGCTGAA GAATTGGATA AGGTATTTAG 1380
 TTTGCTAAAC ATTAACAATA GCCTTTTGGG GAACAAGGGC GCTACTTTTA AGGAAGCCGA 1440
 AGAACATTAC CATATCAATG CTCTTTATCT CTTGCCCCAT AGTGCCCTAG AAAGTAACTG 1500
 GGGAAGAAGT AAAATTGCCA AAGATAAGAA TAATTTCTTT GGCATTACAG CCTATGATAC 1560
 GACCCCTTAC CTTTCTGCTA AGACATTTGA TGATGTGGAT AAGGGAATTT TAGGTGCAAC 1620
 CAAGTGGAAT AAGGAAAATT ATATCGATAG GGGAAGAACT TTCCTTGGA ACAAGGCTTC 1680
 TGGTATGAAT GTGGAATATG CTTAGACCC TTATTGGGGC GAAAAAATTG CTAGTGTGAT 1740
 GATGAAAATC AATGAGAAGC TAGGTGGCAA AGAT 1774

(2) INFORMATION FOR SEQ ID NO:74:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 591 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:74:

Ser Asp Gly Thr Trp Gln Gly Lys Gln Tyr Leu Lys Glu Asp Gly Ser
 1 5 10 15
 Gln Ala Ala Asn Glu Trp Val Xaa Asp Thr His Tyr Gln Ser Trp Phe
 20 25 30
 Tyr Ile Lys Ala Asp Ala Asn Tyr Ala Glu Asn Glu Trp Leu Lys Gln
 35 40 45
 Gly Asp Asp Tyr Phe Tyr Leu Lys Ser Gly Gly Tyr Met Ala Lys Ser
 50 55 60
 Glu Trp Val Glu Asp Lys Gly Ala Phe Tyr Tyr Leu Asp Gln Asp Gly
 65 70 75 80
 Lys Met Lys Arg Asn Ala Trp Val Gly Thr Ser Tyr Val Gly Ala Thr
 85 90 95
 Gly Ala Lys Val Ile Glu Asp Trp Val Tyr Asp Ser Gln Tyr Asp Ala
 100 105 110
 Trp Phe Tyr Ile Lys Ala Asp Gly Gln His Ala Glu Lys Glu Trp Leu
 115 120 125
 Gln Ile Lys Gly Lys Asp Tyr Tyr Phe Lys Ser Gly Gly Tyr Leu Leu
 130 135 140
 Thr Ser Gln Trp Ile Asn Gln Ala Tyr Val Asn Ala Ser Gly Ala Lys
 145 150 155 160
 Val Gln Gln Gly Trp Leu Phe Asp Lys Gln Tyr Gln Ser Trp Phe Tyr
 165 170 175
 Ile Lys Glu Asn Gly Asn Tyr Ala Asp Lys Glu Trp Ile Phe Glu Asn
 180 185 190
 Gly His Tyr Tyr Tyr Leu Lys Ser Gly Gly Tyr Met Ala Ala Asn Glu
 195 200 205
 Trp Ile Trp Asp Lys Glu Ser Trp Phe Tyr Leu Lys Phe Asp Gly Lys
 210 215 220
 Met Ala Glu Lys Glu Trp Val Tyr Asp Ser His Ser Gln Ala Trp Tyr
 225 230 235 240
 Tyr Phe Lys Ser Gly Gly Tyr Met Thr Ala Asn Glu Trp Ile Trp Asp
 245 250 255
 Lys Glu Ser Trp Phe Tyr Leu Lys Ser Asp Gly Lys Ile Ala Glu Lys
 260 265 270
 Glu Trp Val Tyr Asp Ser His Ser Gln Ala Trp Tyr Tyr Phe Lys Ser
 275 280 285
 Gly Gly Tyr Met Ala Lys Asn Glu Thr Val Asp Gly Tyr Gln Leu Gly
 290 295 300
 Ser Asp Gly Lys Trp Leu Gly Gly Lys Thr Thr Asn Glu Asn Ala Ala
 305 310 315 320
 Tyr Tyr Gln Val Val Pro Val Thr Ala Asn Val Tyr Asp Ser Asp Gly
 325 330 335

Glu Lys Leu Ser Tyr Ile Ser Gln Gly Ser Val Val Trp Leu Asp Lys
 340 345 350
 Asp Arg Lys Ser Asp Asp Lys Arg Leu Ala Ile Thr Ile Ser Gly Leu
 355 360 365
 Ser Gly Tyr Met Lys Thr Glu Asp Leu Gln Ala Leu Asp Ala Ser Lys
 370 375 380
 Asp Phe Ile Pro Tyr Tyr Glu Ser Asp Gly His Arg Phe Tyr His Tyr
 385 390 395 400
 Val Ala Gln Asn Ala Ser Ile Pro Val Ala Ser His Leu Ser Asp Met
 405 410 415
 Glu Val Gly Lys Lys Tyr Tyr Ser Ala Asp Gly Leu His Phe Asp Gly
 420 425 430
 Phe Lys Leu Glu Asn Pro Phe Leu Phe Lys Asp Leu Thr Glu Ala Thr
 435 440 445
 Asn Tyr Ser Ala Glu Glu Leu Asp Lys Val Phe Ser Leu Leu Asn Ile
 450 455 460
 Asn Asn Ser Leu Leu Glu Asn Lys Gly Ala Thr Phe Lys Glu Ala Glu
 465 470 475 480
 Glu His Tyr His Ile Asn Ala Leu Tyr Leu Leu Ala His Ser Ala Leu
 485 490 495
 Glu Ser Asn Trp Gly Arg Ser Lys Ile Ala Lys Asp Lys Asn Asn Phe
 500 505 510
 Phe Gly Ile Thr Ala Tyr Asp Thr Thr Pro Tyr Leu Ser Ala Lys Thr
 515 520 525
 Phe Asp Asp Val Asp Lys Gly Ile Leu Gly Ala Thr Lys Trp Ile Lys
 530 535 540
 Glu Asn Tyr Ile Asp Arg Gly Arg Thr Phe Leu Gly Asn Lys Ala Ser
 545 550 555 560
 Gly Met Asn Val Glu Tyr Ala Ser Asp Pro Tyr Trp Gly Glu Lys Ile
 565 570 575
 Ala Ser Val Met Met Lys Ile Asn Glu Lys Leu Gly Gly Lys Asp
 580 585 590

(2) INFORMATION FOR SEQ ID NO: 75:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1105 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 75:

TGGGATTCAA TATGTCAGAG ATGATACTAG AGATAAAGAA GAGGGAATAG AGTATGATGA

CGCTGACAAT GGGGATATTA TTGTAAAAGT AGCGACTAAA CCTAAGGTAG TAACCAAGAA 120
AATTTCAAGT ACGCGAATTC GTTATGAAAA AGATGAAACA AAAGACCGTA GTGAAAATCC 180
TGTTACAATT GATGGAGAGG ATGGCTATGT AACTACGACA AGGACCTACG ATGTTAATCC 240
AGAGACTGGT TATGTTACCG AACAGGTTAC TGTTGATAGA AAAGAAGCCA CGGATACAGT 300
TATCAAAGTT CCAGCTAAAA GCAAGGTTGA AGAAGTTCTT GTTCCATTG CTACTAAATA 360
TGAAGCAGAC AATGACCTTT CTGCAGGACA GGAGCAAGAG ATTACTCTAG GAAAGAATGG 420
GAAAACAGTT ACAACGATAA CTTATAATGT AGATGGAAAG AGTGGACAAG TAACTGAGAG 480
TACTTTAAGT CAAAAAAAG ACTCtCAAAC AAGAGTTGTT AAAAAAGaA CCArkCCCCA 540
AGTTCTTGTC CAAGAAATTC CAATCGAAAC AGAATATCTC GATGGCCCaa CTCTTGATAA 600
AaGTCAAGAA GTAGAAGAAG TAGGAGAAAT TGGTAAATTA CTCTTACTAC AATCTATACT 660
GGTAGATGAA CGTGATGGAA CAATTGAAGA AACTACTTCT CGTCAAATTA CTAAAGAGAT 720
GGTAAAAAGA CGTATAAGGA GAGGGACGAG AGAACCTGAA AAAGTTGTTG TTCCTGAGCA 780
ATCATCTATT CCTTCGTATC CTGTATCTGT TACATCTAAC CAAGGAACAG ATGTAGCAGT 840
AGAACCAGCT AAAGCAGTTG CTCCAACAAC AGACTGGAAA CAAGAAAATG GTATGTGGTA 900
TTTTTATAAT ACTGATGGTT CCATGGCAAC AGGTTGGGTA CAAGTTAATA GTTCATGGTA 960
CTACCTCAAC AGCAACGGTT CTATGAAAGT CAATCAATGG TTCCAAGTTG GTGGTAAATG 1020
GTATTATGTA AATACATCGG GTGAGTTAGC GGTCAATACA AGTATAGATG GCTATAGAGT 1080
CAATGATAAT GGTGAATGGG TGCCT 1105

(2) INFORMATION FOR SEQ ID NO:76:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 368 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:76:

Gly Ile Gln Tyr Val Arg Asp Asp Thr Arg Asp Lys Glu Glu Gly Ile
1 5 10 15
Glu Tyr Asp Asp Ala Asp Asn Gly Asp Ile Ile Val Lys Val Ala Thr
20 25 30
Lys Pro Lys Val Val Thr Lys Lys Ile Ser Ser Thr Arg Ile Arg Tyr
35 40 45
Glu Lys Asp Glu Thr Lys Asp Arg Ser Glu Asn Pro Val Thr Ile Asp
50 55 60
Gly Glu Asp Gly Tyr Val Thr Thr Thr Arg Thr Tyr Asp Val Asn Pro
65 70 75 80

Glu Thr Gly Tyr Val Thr Glu Gln Val Thr Val Asp Arg Lys Glu Ala
 85 90 95
 Thr Asp Thr Val Ile Lys Val Pro Ala Lys Ser Lys Val Glu Glu Val
 100 105 110
 Leu Val Pro Phe Ala Thr Lys Tyr Glu Ala Asp Asn Asp Leu Ser Ala
 115 120 125
 Gly Gln Glu Gln Glu Ile Thr Leu Gly Lys Asn Gly Lys Thr Val Thr
 130 135 140
 Thr Ile Thr Tyr Asn Val Asp Gly Lys Ser Gly Gln Val Thr Glu Ser
 145 150 155 160
 Thr Leu Ser Gln Lys Lys Asp Ser Gln Thr Arg Val Val Lys Lys Arg
 165 170 175
 Thr Xaa Pro Gln Val Leu Val Gln Glu Ile Pro Ile Glu Thr Glu Tyr
 180 185 190
 Leu Asp Gly Pro Thr Leu Asp Lys Ser Gln Glu Val Glu Glu Val Gly
 195 200 205
 Glu Ile Gly Lys Leu Leu Leu Leu Gln Ser Ile Leu Val Asp Glu Arg
 210 215 220
 Asp Gly Thr Ile Glu Glu Thr Thr Ser Arg Gln Ile Thr Lys Glu Met
 225 230 235 240
 Val Lys Arg Arg Ile Arg Arg Gly Thr Arg Glu Pro Glu Lys Val Val
 245 250 255
 Val Pro Glu Gln Ser Ser Ile Pro Ser Tyr Pro Val Ser Val Thr Ser
 260 265 270
 Asn Gln Gly Thr Asp Val Ala Val Glu Pro Ala Lys Ala Val Ala Pro
 275 280 285
 Thr Thr Asp Trp Lys Gln Glu Asn Gly Met Trp Tyr Phe Tyr Asn Thr
 290 295 300
 Asp Gly Ser Met Ala Thr Gly Trp Val Gln Val Asn Ser Ser Trp Tyr
 305 310 315 320
 Tyr Leu Asn Ser Asn Gly Ser Met Lys Val Asn Gln Trp Phe Gln Val
 325 330 335
 Gly Gly Lys Trp Tyr Tyr Val Asn Thr Ser Gly Glu Leu Ala Val Asn
 340 345 350
 Thr Ser Ile Asp Gly Tyr Arg Val Asn Asp Asn Gly Glu Trp Val Arg
 355 360 365

(2) INFORMATION FOR SEQ ID NO: 77:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 661 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 77:

GGATAATAGA GAAGCATTAA AACCTTTTAT GACGGGTGAA AATTTTATC TCCAACATTA 60
 TCTAGGAGCA CATAGGGAAG AACTAAATGG AGAGCATGGC TATACCTTCC GTGTTTGGGC 120
 ACCTAATGCT CAGGCTGTTC ACTTGGTTGG TGATTTTACC AACTGGATTG AAAATCAGAT 180
 TCCAATGGTA AGAAATGATT TTGGGGTCTG GGAAGTCTTT ACCAATATGG CTCAAGAAGG 240
 GCATATTTAC AAATATCATG TCACACGTCA AAATGGTCAT CAACTGATGA AGATTGACCC 300
 TTTTGCTGTC AGGTATGAGG CTCGTCCAGG AACAGGGGCA ATCGTAACAG AGCTTCCTGA 360
 GAAGAAATGG AAGGATGGAC TT'TGGCTGGC ACGAAGAAAA CGTTGGGGCT TTGAAGAGCG 420
 TCCTGTCAAT ATTTATGAAG TTCACGCTGG ATCATGGAAA AGAAATTCTG ATGGCAGTCC 480
 TTATAGTTTT GCCCAGCTCA AGGATGAACT CATTCTTAT CTCGTTGAAA TGAACATAC 540
 TCATATTGAG TTTATGCCCT TGATGTCCCA TCCTTTGGGC TTGAGTTGGG GGTATCAGCT 600
 TATGGGTAC TTCGCTTTAG AGCATGCTTA TGGCCGACCA GAGGAGTTTC AAGATTTTGT 660
 C 661

(2) INFORMATION FOR SEQ ID NO:78:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 220 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:78:

Asp Asn Arg Glu Ala Leu Lys Thr Phe Met Thr Gly Glu Asn Phe Tyr
 1 5 10 15
 Leu Gln His Tyr Leu Gly Ala His Arg Glu Glu Leu Asn Gly Glu His
 20 25 30
 Gly Tyr Thr Phe Arg Val Trp Ala Pro Asn Ala Gln Ala Val His Leu
 35 40 45
 Val Gly Asp Phe Thr Asn Trp Ile Glu Asn Gln Ile Pro Met Val Arg
 50 55 60
 Asn Asp Phe Gly Val Trp Glu Val Phe Thr Asn Met Ala Gln Glu Gly
 65 70 75 80
 His Ile Tyr Lys Tyr His Val Thr Arg Gln Asn Gly His Gln Leu Met
 85 90 95
 Lys Ile Asp Pro Phe Ala Val Arg Tyr Glu Ala Arg Pro Gly Thr Gly
 100 105 110
 Ala Ile Val Thr Glu Leu Pro Glu Lys Lys Trp Lys Asp Gly Leu Trp

115	120	125
Leu Ala Arg Arg Lys Arg Trp Gly Phe Glu Glu Arg Pro Val Asn Ile		
130	135	140
Tyr Glu Val His Ala Gly Ser Trp Lys Arg Asn Ser Asp Gly Ser Pro		
145	150	155
Tyr Ser Phe Ala Gln Leu Lys Asp Glu Leu Ile Pro Tyr Leu Val Glu		
165	170	175
Met Asn Tyr Thr His Ile Glu Phe Met Pro Leu Met Ser His Pro Leu		
180	185	190
Gly Leu Ser Trp Gly Tyr Gln Leu Met Gly Tyr Phe Ala Leu Glu His		
195	200	205
Ala Tyr Gly Arg Pro Glu Glu Phe Gln Asp Phe Val		
210	215	220

(2) INFORMATION FOR SEQ ID NO: 79:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 976 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 79:

AGATTTTGTC GAGGAGTGTC ATACCCATAA TATTGGGGTT ATTGTGGACT GGGTACCAGN	60
TCACTTTACC ATCAACGATG ATGCCTTAGC CTATTATGAT GGGACACCGA CTTTGAATA	120
CCAAGACCAT AATAAGGCTC ATAACCATGG TTGGGGTGCC CTTAATTTTG ACCTTGAAAA	180
AAATGAAGTC CAGTCCTTCT TAATTTCTTG CATTAAGCAT TGGATTGATG TCTATCATT	240
GGATGGTATT CGTGTGGATG CTGTTAGCAA CATGCTCTAT TTGGACTATG ATGATGCTCC	300
ATGGACACCT AATAAAGATG GCGGAAATCT CAACTATGAA GGTTATTATT TCCTTCAGCG	360
CTTGAATGAG GTTATTAAGT TAGAATATCC AGATGTGATG ATGATTGCAG AAGAAAGTTC	420
GTCTGCGATC AAGATTACGG GAATGAAAGA GATTGGTGGT CTAGGATTTG ACTACAAATG	480
GAACATGGGC TGGATGAATG ATATCCTCCG TTTCTACGAA GAAGATCCGA TCTATCGTAA	540
ATATGACTTT AACCTGGTGA CTTTCAGCTT TATGTATGTT TNCAAGGAGA ATTATCTCTT	600
GCCATTCTCG CACGATGAAG TGGTTCATGG CAAGAAGAGT ATGATGCATA AGATGTGGGG	660
AGATCGTTAC AATCAATTCG CAGGCTTGCG CAATCTCTAT ACGTACCAA TTTGTCACCC	720
TGGTAAGAAA TTGCTCTTCA TGGGTAGCGA ATACGGTCAA TTCCTAGAAT GGAAATCTGA	780
AGAACAGTTG GAATGGTCTA ACCTAGAAGA CCCAATGAAT GCTAAGATGA AGTATTTTCGC	840
TTCTCAGCTA AACCAGTTTT ACAAGATCA TCGCTGTCTG TGGGAAATG ATACCAGCTA	900
TGATGGTATT GAAATCATTG ATGCGGATAA TCGAGACCAG AGTGTCTCTT CTTTATTTCG	960

TAAGGGTAAA AAGGGA

976

(2) INFORMATION FOR SEQ ID NO:80:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 325 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:80:

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Asp Phe Val Glu Glu Cys His Thr His Asn Ile Gly Val Ile Val Asp
1           5           10           15

Trp Val Pro Xaa His Phe Thr Ile Asn Asp Asp Ala Leu Ala Tyr Tyr
          20           25           30

Asp Gly Thr Pro Thr Phe Glu Tyr Gln Asp His Asn Lys Ala His Asn
          35           40           45

His Gly Trp Gly Ala Leu Asn Phe Asp Leu Gly Lys Asn Glu Val Gln
          50           55           60

Ser Phe Leu Ile Ser Cys Ile Lys His Trp Ile Asp Val Tyr His Leu
65           70           75           80

Asp Gly Ile Arg Val Asp Ala Val Ser Asn Met Leu Tyr Leu Asp Tyr
          85           90           95

Asp Asp Ala Pro Trp Thr Pro Asn Lys Asp Gly Gly Asn Leu Asn Tyr
          100          105          110

Glu Gly Tyr Tyr Phe Leu Gln Arg Leu Asn Glu Val Ile Lys Leu Glu
          115          120          125

Tyr Pro Asp Val Met Met Ile Ala Glu Glu Ser Ser Ser Ala Ile Lys
          130          135          140

Ile Thr Gly Met Lys Glu Ile Gly Gly Leu Gly Phe Asp Tyr Lys Trp
145          150          155          160

Asn Met Gly Trp Met Asn Asp Ile Leu Arg Phe Tyr Glu Glu Asp Pro
          165          170          175

Ile Tyr Arg Lys Tyr Asp Phe Asn Leu Val Thr Phe Ser Phe Met Tyr
          180          185          190

Val Xaa Lys Glu Asn Tyr Leu Leu Pro Phe Ser His Asp Glu Val Val
          195          200          205

His Gly Lys Lys Ser Met Met His Lys Met Trp Gly Asp Arg Tyr Asn
          210          215          220

Gln Phe Ala Gly Leu Arg Asn Leu Tyr Thr Tyr Gln Ile Cys His Pro
225          230          235          240

Gly Lys Lys Leu Leu Phe Met Gly Ser Glu Tyr Gly Gln Phe Leu Glu
          245          250          255

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F00001.0 12299260

Trp Lys Ser Glu Glu Gln Leu Glu Trp Ser Asn Leu Glu Asp Pro Met
 260 265 270

Asn Ala Lys Met Lys Tyr Phe Ala Ser Gln Leu Asn Gln Phe Tyr Lys
 275 280 285

Asp His Arg Cys Leu Trp Glu Ile Asp Thr Ser Tyr Asp Gly Ile Glu
 290 295 300

Ile Ile Asp Ala Asp Asn Arg Asp Gln Ser Val Leu Ser Phe Ile Arg
 305 310 315 320

Lys Gly Lys Lys Gly
 325

(2) INFORMATION FOR SEQ ID NO: 81:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2134 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 81:

ATCTGTAGTT TATGCGGATG AAACACTTAT TACTCATACT GCTGAGAAAC CTAAAGAGGA	60
AAAAATGATA GTAGAAGAAA AGGCTGATAA AGCTTTGGAA ACTAAAAATA TAGTTGAAAG	120
GACAGAACAA AGTGAACCTA GTTCAACTGA GGCTATTGCA TCTGAGNAGA AAGAAGATGA	180
AGCCGTA ACT CCAAAGAGG AAAAAGTGTC TGCTAAACCG GAAGAAAAAG CTCCAAGGAT	240
AGAATCACAA GCTTCAAATC AAGAAAAACC GCTCAAGGAA GATGCTAAAG CTGTAACAAA	300
TGAAGAAGTG AATCAAATGA TTGAAGACAG GAAAGTGGAT TTTAATCAAA ATTGGTACTT	360
TAAACTCAAT GCAAATTCTA AGGAAGCCAT TAAACCTGAT GCAGACGTAT CTACGTGGAA	420
AAAATTAGAT TTACCGTATG ACTGGAGTAT CTTTAACGAT TTCGATCATG AATCTCCTGC	480
ACAAATGAA GGTGGACAGC TCAACGGTGG GGAAGCTTGG TATCGCAAGA CTTTCAA ACT	540
AGATGAAAAA GACCTCAAGA AAAATGTTCG CCTTACTTTT GATGGCGTCT ACATGGATTC	600
TCAAGTTTAT GTCAATGGTC AGTTAGTGGG GCATTATCCA AATGGTTATA ACCAGTTCTC	660
ATATGATATC ACCAAATACC TTCAAAAAGA TGGTCGTGAG AATGTGATTG CTGTCCATGC	720
AGTCAACAAA CAGCCAAGTA GCCGTTGGTA TTCAGGAAGT GGTATCTATC GTGATGTGAC	780
TTTACAAGTG ACAGATAAGG TGCATGTTGA GAAAAATGGG ACAACTATTT TAACACCAAA	840
ACTTGAAGAA CAACAACATG GCAAGGTTGA AACTCATGTG ACCAGCAAAA TCGTCAATAC	900
GGACGACAAA GACCATGAAC TTGTAGCCGA ATATCAAATC GTTGAACGAG GTGGTCATGC	960
TGTAACAGGC TTAGTTCGTA CAGCGAGTCG TACCTTAAAA GCACATGAAT CAACAAGCCT	1020
AGATGCGATT TTAGAAGTTG AAAGACCAA ACTCTGGACT GTTTTAAATG ACAAACCTGC	1080

CTTGTACGAA TTGATTACGC GTGTTTACCG TGACGGTCAA TTGGTTGATG CTAAGAAGGA 1140
 TTTGTTTGGT TACCGTTACT ATCACTGGAC TCCAAATGAA GGTTCCTCTT TGAATGGTGA 1200
 ACGTATTAAA TTCCATGGAG TATCCTTGCA CCACGACCAT GGGGCGCTTG GAGCAGAAGA 1260
 AAACTATAAA GCAGAATATC GCCGTCTCAA ACAAATGAAG GAGATGGGAG TTAAGTCCAT 1320
 CCGTACAACC CACAACCCTG CTAGTGAGCA AACCTTGCAA ATCGCAGCAG AACTAGGTTT 1380
 ACTCGTTCAG GAAGAGGCCT TTGATACGTG GTATGGTGGC AAGAAACCTT ATGACTATGG 1440
 ACGTTTCTTT GAAAAAGATG CCACTCACCC AGAAGCTCGA AAAGGTGAAA AATGGTCTGA 1500
 TTTTGACCTA CGTACCATGG TCGAAAGAGG CAAAACAAC CCTGCTATCT TCATGTGGTC 1560
 AATTGGTAAT GAAATAGGTG AAGCTAATGG TGATGCCAC TCTTTAGCAA CTGTAAACG 1620
 TTTGGTTAAG GTTATCAAGG ATGTTGATAA GACTCGCTAT GTTACCATGG GAGCAGATAA 1680
 ATTCCGTTTC GGTAATGGTA GCGGAGGGCA TGAGAAAATT GCTGATGAAC TCGATGCTGT 1740
 TGGATTTAAC TATTCTGAAG ATAATTACAA AGCCCTTAGA GCTAAGCATC CAAAATGGTT 1800
 GATTTATGGA TCAGAAACAT CTTACAGCTAC CCGTACACGT GGAAGTTACT ATCGCCCTGA 1860
 ACGTGAATTG AAACATAGCA ATGGACCTGA GCGTAATTAT GAACAGTCAG ATTATGGAAA 1920
 TGATCGTGTG GGTGAGGGGA AAACAGCAAC CGCTTCATGG ACTTTTGACC GTGACAACGC 1980
 TGGCTATGCT GGACAGTTTA TCTGGACAGG TACGGACTAT ATTGGTGAAC CTACACCATG 2040
 GCACAACCAA AATCAAACCT CTGTTAAGAG CTCTTACTTT GGTATCGTAG ATACAGCCGG 2100
 CATTCACAAA CATGACTTCT ATCTCTACCA AAGC 2134

(2) INFORMATION FOR SEQ ID NO:82:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 711 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:82:

Ser Val Val Tyr Ala Asp Glu Thr Leu Ile Thr His Thr Ala Glu Lys
 1 5 10 15
 Pro Lys Glu Glu Lys Met Ile Val Glu Glu Lys Ala Asp Lys Ala Leu
 20 25 30
 Glu Thr Lys Asn Ile Val Glu Arg Thr Glu Gln Ser Glu Pro Ser Ser
 35 40 45
 Thr Glu Ala Ile Ala Ser Glu Xaa Lys Glu Asp Glu Ala Val Thr Pro
 50 55 60
 Lys Glu Glu Lys Val Ser Ala Lys Pro Glu Glu Lys Ala Pro Arg Ile

65						70						75						80
Glu	Ser	Gln	Ala	Ser	Asn	Gln	Glu	Lys	Pro	Leu	Lys	Glu	Asp	Ala	Lys			
				85					90					95				
Ala	Val	Thr	Asn	Glu	Glu	Val	Asn	Gln	Met	Ile	Glu	Asp	Arg	Lys	Val			
			100					105					110					
Asp	Phe	Asn	Gln	Asn	Trp	Tyr	Phe	Lys	Leu	Asn	Ala	Asn	Ser	Lys	Glu			
		115					120					125						
Ala	Ile	Lys	Pro	Asp	Ala	Asp	Val	Ser	Thr	Trp	Lys	Lys	Leu	Asp	Leu			
	130					135					140							
Pro	Tyr	Asp	Trp	Ser	Ile	Phe	Asn	Asp	Phe	Asp	His	Glu	Ser	Pro	Ala			
145					150				155						160			
Gln	Asn	Glu	Gly	Gly	Gln	Leu	Asn	Gly	Gly	Glu	Ala	Trp	Tyr	Arg	Lys			
			165					170						175				
Thr	Phe	Lys	Leu	Asp	Glu	Lys	Asp	Leu	Lys	Lys	Asn	Val	Arg	Leu	Thr			
			180					185					190					
Phe	Asp	Gly	Val	Tyr	Met	Asp	Ser	Gln	Val	Tyr	Val	Asn	Gly	Gln	Leu			
		195					200					205						
Val	Gly	His	Tyr	Pro	Asn	Gly	Tyr	Asn	Gln	Phe	Ser	Tyr	Asp	Ile	Thr			
	210					215					220							
Lys	Tyr	Leu	Gln	Lys	Asp	Gly	Arg	Glu	Asn	Val	Ile	Ala	Val	His	Ala			
225				230					235					240				
Val	Asn	Lys	Gln	Pro	Ser	Ser	Arg	Trp	Tyr	Ser	Gly	Ser	Gly	Ile	Tyr			
			245					250						255				
Arg	Asp	Val	Thr	Leu	Gln	Val	Thr	Asp	Lys	Val	His	Val	Glu	Lys	Asn			
		260						265					270					
Gly	Thr	Thr	Ile	Leu	Thr	Pro	Lys	Leu	Glu	Glu	Gln	Gln	His	Gly	Lys			
		275				280						285						
Val	Glu	Thr	His	Val	Thr	Ser	Lys	Ile	Val	Asn	Thr	Asp	Asp	Lys	Asp			
	290					295					300							
His	Glu	Leu	Val	Ala	Glu	Tyr	Gln	Ile	Val	Glu	Arg	Gly	Gly	His	Ala			
305				310						315				320				
Val	Thr	Gly	Leu	Val	Arg	Thr	Ala	Ser	Arg	Thr	Leu	Lys	Ala	His	Glu			
			325					330						335				
Ser	Thr	Ser	Leu	Asp	Ala	Ile	Leu	Glu	Val	Glu	Arg	Pro	Lys	Leu	Trp			
		340					345						350					
Thr	Val	Leu	Asn	Asp	Lys	Pro	Ala	Leu	Tyr	Glu	Leu	Ile	Thr	Arg	Val			
		355				360						365						
Tyr	Arg	Asp	Gly	Gln	Leu	Val	Asp	Ala	Lys	Lys	Asp	Leu	Phe	Gly	Tyr			
	370				375						380							
Arg	Tyr	Tyr	His	Trp	Thr	Pro	Asn	Glu	Gly	Phe	Ser	Leu	Asn	Gly	Glu			
385					390					395					400			
Arg	Ile	Lys	Phe	His	Gly	Val	Ser	Leu	His	His	Asp	His	Gly	Ala	Leu			

405

410

415

Gly Ala Glu Glu Asn Tyr Lys Ala Glu Tyr Arg Arg Leu Lys Gln Met
420 425 430

Lys Glu Met Gly Val Asn Ser Ile Arg Thr Thr His Asn Pro Ala Ser
435 440 445

Glu Gln Thr Leu Gln Ile Ala Ala Glu Leu Gly Leu Leu Val Gln Glu
450 455 460

Glu Ala Phe Asp Thr Trp Tyr Gly Gly Lys Lys Pro Tyr Asp Tyr Gly
465 470 475 480

Arg Phe Phe Glu Lys Asp Ala Thr His Pro Glu Ala Arg Lys Gly Glu
485 490 495

Lys Trp Ser Asp Phe Asp Leu Arg Thr Met Val Glu Arg Gly Lys Asn
500 505 510

Asn Pro Ala Ile Phe Met Trp Ser Ile Gly Asn Glu Ile Gly Glu Ala
515 520 525

Asn Gly Asp Ala His Ser Leu Ala Thr Val Lys Arg Leu Val Lys Val
530 535 540

Ile Lys Asp Val Asp Lys Thr Arg Tyr Val Thr Met Gly Ala Asp Lys
545 550 555 560

Phe Arg Phe Gly Asn Gly Ser Gly Gly His Glu Lys Ile Ala Asp Glu
565 570 575

Leu Asp Ala Val Gly Phe Asn Tyr Ser Glu Asp Asn Tyr Lys Ala Leu
580 585 590

Arg Ala Lys His Pro Lys Trp Leu Ile Tyr Gly Ser Glu Thr Ser Ser
595 600 605

Ala Thr Arg Thr Arg Gly Ser Tyr Tyr Arg Pro Glu Arg Glu Leu Lys
610 615 620

His Ser Asn Gly Pro Glu Arg Asn Tyr Glu Gln Ser Asp Tyr Gly Asn
625 630 635 640

Asp Arg Val Gly Trp Gly Lys Thr Ala Thr Ala Ser Trp Thr Phe Asp
645 650 655

Arg Asp Asn Ala Gly Tyr Ala Gly Gln Phe Ile Trp Thr Gly Thr Asp
660 665 670

Tyr Ile Gly Glu Pro Thr Pro Trp His Asn Gln Asn Gln Thr Pro Val
675 680 685

Lys Ser Ser Tyr Phe Gly Ile Val Asp Thr Ala Gly Ile Pro Lys His
690 695 700

Asp Phe Tyr Leu Tyr Gln Ser
705 710

(2) INFORMATION FOR SEQ ID NO: 83:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 2167 base pairs

006324 04300

(B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 83:

TTACTTTGGT ATCGTAGATA CAGCCGGCAT TCCAAAACAT GACTTCTATC TCTACCAAAG	60
CCAATGGGTT TCTGTTAAGA AGAAACCGAT GGTACACCTT CTTCTCACT GGAAGTGGGA	120
AAACAAAGAA TTAGCATCCA AAGTAGCTGA CTCAGAAGGT AAGATTCCAG TTCGTGCTTA	180
TTCGAATGCT TCTAGTGTAG AATTGTTCTT GAATGGAAAA TCTCTTGGTC TTAAGACTTT	240
CAATAAAAAA CAAACCAGCG ATGGGCGGAC TTACCAAGAA GGTGCAATG CTAATGAACT	300
TTATCTTGAA TGGAAAGTTG CCTATCAACC AGGTACCTTG GAAGCAATTG CTCGTGATGA	360
ATCTGGCAAG GAAATTGCTC GAGATAAGAT TACGACTGCT GGTAAGCCAG CGGCAGTTTCG	420
TCTTATTAAG GAAGACCATG CGATTGCAGC AGATGGAAAA GACTTGACTT ACATCTACTA	480
TGAAATTGTT GACAGCCAGG GGAATGTGGT TCCAAGTCTG AATAATCTGG TTCGCTTCCA	540
ATTGCATGGC CAAGGTCAAC TGGTCGGTGT AGATAACGGA GAACAAGCCA GCCGTGAACG	600
CTATAAGGCG CAAGCAGATG GTTCTTGGAT TCGTAAAGCA TTTAATGGTA AAGGTGTTGC	660
CATTGTCAAA TCAACTGAAC AAGCAGGGAA ATTCACCCTG ACTGCCCCACT CTGATCTCTT	720
GAAATCGAAC CAAGTCACTG TCTTTACTGG TAAGAAAGAA GGACAAGAGA AGACTGTTTT	780
GGGGACAGAA GTGCCAAAAG TACAGACCAT TATTGGAGAG GCACCTGAAA TGCCTACCAC	840
TGTTCCGTTT GTATACAGTG ATGGTAGCCG TGCAGAACGT CCTGTAACCT GGTCTTCAGT	900
AGATGTGAGC AAGCCTGGTA TTGTAACGGT GAAAGGTATG GCTGACGGAC GAGAAGTAGA	960
AGCTCGTGTA GAAGTGATTG CTCTTAAATC AGAGCTACCA GTTGTGAAAC GTATTGCTCC	1020
AAATACTGAC TTGAATTCTG TAGACAAATC TGTTTCCTAT GTTTTGATTG ATGGAAGTGT	1080
TGAAGAGTAT GAAGTGGACA AGTGGGAGAT TGCCGAAGAA GATAAAGCTA AGTTAGCAAT	1140
TCCAGGTTCT CGTATTCAAG CGACCGGTTA TTTAGAAGGT CAACCAATTC ATGCAACCCCT	1200
TGTGGTAGAA GAAGGCAATC CTGCGGCACC TGCAGTACCA ACTGTAACGG TTGGTGGTGA	1260
GGCAGTAACA GGTCTTACTA GTCAAAAACC AATGCAATAC CGCACTCTTG CTTATGGAGC	1320
TAAGTTGCCA GAAGTCACAG CAAGTGCTAA AAATGCAGCT GTTACAGTTC TTCAAGCAAG	1380
CGCAGCAAAC GGCATGCGTG CGAGCATCTT TATTACAGCT AAAGATGGTG GCCCTCTTCA	1440
AACCTATGCA ATTCAATTCC TTGAAGAAGC GCCAAAATTT GCTCACTTGA GCTTGCAAGT	1500
GGAAAAAGCT GACAGTCTCA AAGAAGACCA AACTGTCAAA TTGTCGGTTC GAGCTCACTA	1560
TCAAGATGGA ACGCAAGCTG TATTACCAGC TGATAAAGTA ACCTTCTCTA CAAGTGGTGA	1620
AGGGGAAGTC GCAATTCGTA AAGGAATGCT TGAGTTGCAT AAGCCAGGAG CAGTCACTCT	1680

GAACGCTGAA TATGAGGGAG CTAAAGACCA AGTTGAACTC ACTATCCAAG CCAATACTGA 1740
 GAAGAAGATT GCGCAATCCA TCCGTCCTGT AAATGTAGTG ACAGATTTGC ATCAGGAACC 1800
 AAGTCTTCCA GCAACAGTAA CAGTTGAGTA TGACAAAGGT TTCCCTAAAA CTCATAAAGT 1860
 CACTTGGCAA GCTATTCCGA AAGAAAACT AGACTCCTAT CAAACATTTG AAGTACTAGG 1920
 TAAAGTTGAA GGAATTGACC TTGAAGCGCG TGCAAAAGTC TCTGTAGAAG GTATCGTTTC 1980
 AGTTGAAGAA GTCAGTGTGA CAACTCCAAT CGCAGAAGCA CCACAATTAC CAGAAAGTGT 2040
 TCGGACATAT GATTCAAATG GTCACGTTTC ATCAGCTAAG GTTGCATGGG ATGCGATTCTG 2100
 TCCAGAGCAA TACGCTAAGG AAGGTGTCTT TACAGTTAAT GGTGCTTAG AAGGTACGCA 2160
 ATTAACA 2167

(2) INFORMATION FOR SEQ ID NO:84:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 722 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:84:

Tyr Phe Gly Ile Val Asp Thr Ala Gly Ile Pro Lys His Asp Phe Tyr
 1 5 10 15
 Leu Tyr Gln Ser Gln Trp Val Ser Val Lys Lys Lys Pro Met Val His
 20 25 30
 Leu Leu Pro His Trp Asn Trp Glu Asn Lys Glu Leu Ala Ser Lys Val
 35 40 45
 Ala Asp Ser Glu Gly Lys Ile Pro Val Arg Ala Tyr Ser Asn Ala Ser
 50 55 60
 Ser Val Glu Leu Phe Leu Asn Gly Lys Ser Leu Gly Leu Lys Thr Phe
 65 70 75 80
 Asn Lys Lys Gln Thr Ser Asp Gly Arg Thr Tyr Gln Glu Gly Ala Asn
 85 90 95
 Ala Asn Glu Leu Tyr Leu Glu Trp Lys Val Ala Tyr Gln Pro Gly Thr
 100 105 110
 Leu Glu Ala Ile Ala Arg Asp Glu Ser Gly Lys Glu Ile Ala Arg Asp
 115 120 125
 Lys Ile Thr Thr Ala Gly Lys Pro Ala Ala Val Arg Leu Ile Lys Glu
 130 135 140
 Asp His Ala Ile Ala Ala Asp Gly Lys Asp Leu Thr Tyr Ile Tyr Tyr
 145 150 155 160
 Glu Ile Val Asp Ser Gln Gly Asn Val Val Pro Thr Ala Asn Asn Leu

165										170					175						
Val	Arg	Phe	Gln	Leu	His	Gly	Gln	Gly	Gln	Leu	Val	Gly	Val	Asp	Asn						
			180						185					190							
Gly	Glu	Gln	Ala	Ser	Arg	Glu	Arg	Tyr	Lys	Ala	Gln	Ala	Asp	Gly	Ser						
		195					200					205									
Trp	Ile	Arg	Lys	Ala	Phe	Asn	Gly	Lys	Gly	Val	Ala	Ile	Val	Lys	Ser						
	210					215					220										
Thr	Glu	Gln	Ala	Gly	Lys	Phe	Thr	Leu	Thr	Ala	His	Ser	Asp	Leu	Leu						
225					230					235					240						
Lys	Ser	Asn	Gln	Val	Thr	Val	Phe	Thr	Gly	Lys	Lys	Glu	Gly	Gln	Glu						
				245					250					255							
Lys	Thr	Val	Leu	Gly	Thr	Glu	Val	Pro	Lys	Val	Gln	Thr	Ile	Ile	Gly						
			260					265					270								
Glu	Ala	Pro	Glu	Met	Pro	Thr	Thr	Val	Pro	Phe	Val	Tyr	Ser	Asp	Gly						
		275					280					285									
Ser	Arg	Ala	Glu	Arg	Pro	Val	Thr	Trp	Ser	Ser	Val	Asp	Val	Ser	Lys						
	290					295					300										
Pro	Gly	Ile	Val	Thr	Val	Lys	Gly	Met	Ala	Asp	Gly	Arg	Glu	Val	Glu						
305					310					315					320						
Ala	Arg	Val	Glu	Val	Ile	Ala	Leu	Lys	Ser	Glu	Leu	Pro	Val	Val	Lys						
				325					330					335							
Arg	Ile	Ala	Pro	Asn	Thr	Asp	Leu	Asn	Ser	Val	Asp	Lys	Ser	Val	Ser						
			340					345					350								
Tyr	Val	Leu	Ile	Asp	Gly	Ser	Val	Glu	Glu	Tyr	Glu	Val	Asp	Lys	Trp						
		355					360					365									
Glu	Ile	Ala	Glu	Glu	Asp	Lys	Ala	Lys	Leu	Ala	Ile	Pro	Gly	Ser	Arg						
	370					375					380										
Ile	Gln	Ala	Thr	Gly	Tyr	Leu	Glu	Gly	Gln	Pro	Ile	His	Ala	Thr	Leu						
385					390					395					400						
Val	Val	Glu	Glu	Gly	Asn	Pro	Ala	Ala	Pro	Ala	Val	Pro	Thr	Val	Thr						
				405					410					415							
Val	Gly	Gly	Glu	Ala	Val	Thr	Gly	Leu	Thr	Ser	Gln	Lys	Pro	Met	Gln						
			420					425					430								
Tyr	Arg	Thr	Leu	Ala	Tyr	Gly	Ala	Lys	Leu	Pro	Glu	Val	Thr	Ala	Ser						
		435																			

202

500

505

510

Lys Leu Ser Val Arg Ala His Tyr Gln Asp Gly Thr Gln Ala Val Leu
515 520 525

Pro Ala Asp Lys Val Thr Phe Ser Thr Ser Gly Glu Gly Glu Val Ala
530 535 540

Ile Arg Lys Gly Met Leu Glu Leu His Lys Pro Gly Ala Val Thr Leu
545 550 555 560

Asn Ala Glu Tyr Glu Gly Ala Lys Asp Gln Val Glu Leu Thr Ile Gln
565 570 575

Ala Asn Thr Glu Lys Lys Ile Ala Gln Ser Ile Arg Pro Val Asn Val
580 585 590

Val Thr Asp Leu His Gln Glu Pro Ser Leu Pro Ala Thr Val Thr Val
595 600 605

Glu Tyr Asp Lys Gly Phe Pro Lys Thr His Lys Val Thr Trp Gln Ala
610 615 620

Ile Pro Lys Glu Lys Leu Asp Ser Tyr Gln Thr Phe Glu Val Leu Gly
625 630 635 640

Lys Val Glu Gly Ile Asp Leu Glu Ala Arg Ala Lys Val Ser Val Glu
645 650 655

Gly Ile Val Ser Val Glu Glu Val Ser Val Thr Thr Pro Ile Ala Glu
660 665 670

Ala Pro Gln Leu Pro Glu Ser Val Arg Thr Tyr Asp Ser Asn Gly His
675 680 685

Val Ser Ser Ala Lys Val Ala Trp Asp Ala Ile Arg Pro Glu Gln Tyr
690 695 700

Ala Lys Glu Gly Val Phe Thr Val Asn Gly Arg Leu Glu Gly Thr Gln
705 710 715 720

Leu Thr

(2) INFORMATION FOR SEQ ID NO: 85:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2329 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 85:

AGCTAAGGTT GCATGGGATG CGATTCTGCC AGAGCAATAC GCTAAGGAAG GTGTCTTTAC	60
AGTTAATGGT CGCTTAGAAG GTACGCAATT AACAACTAAA CTTTCATGTTT GCGTATCTGC	120
TCAAAGTGAG CAAGGTGCAA ACATTTCTGA CCAATGGACC GGTTCAGAAT TGCCACTTGC	180
CTTTGCTTCA GACTCAAATC CAAGCGACCC AGTTTCAAAT GTTAATGACA AGCTCATTTT	240

CTACAATAAC CAACCAGCCA ATCGTTGGAC AAACCTGGAAT CGTACTAATC CAGAAGCTTC	300
AGTCGGTGTT CTGTTTGGAG ATTCAGGTAT CTTGAGCAAA CGCTCCGTTG ATAATCTAAG	360
TGTCGGATT C CATGAAGACC ATGGAGTTGG TGTACCGAAG TCTTATGTGA TTGAGTATTA	420
TGTTGGTAAG ACTGTCCCAA CAGCTCCTAA AAACCTAGT TTTGTTGGTA ATGAGGACCA	480
TGTCTTTAAT GATTCTGCCA ACTGGAAACC AGTTACTAAT CTAAAAGCCC CTGCTCAACT	540
CAAGGCTGGA GAAATGAACC ACTTTAGCTT TGATAAAGTT GAAACCTATG CTGTTCTGTAT	600
TCGCATGGTT AAAGCAGATA ACAAGCGTGG AACGTCTATC ACAGAGGTAC AAATCTTTGC	660
GAAACAAGTT GCGGCAGCCA AGCAAGGACA AACAAGAATC CAAGTTGACG GCAAAGACTT	720
AGCAAACCTC AACCTTGATT TGACAGACTA CTACCTTGAG TCTGTAGATG GAAAAGTTCC	780
GGCAGTCACA GCAAGTGTTA GCAACAATGG TCTCGCTACC GTCGTTCCAA GCGTTCGTGA	840
AGGTGAGCCA GTTCGTGTCA TCGCGAAAGC TGAAAATGGC GACATCTTAG GAGAATACCG	900
TCTGCACTTC ACTAAGGATA AGAGCTTACT TTCTCATAAA CCAGTTGCTG CGGTAAACA	960
AGCTCGCTTG CTACAAGTAG GTCAAGCACT TGAATTGCCG ACTAAGGTTT CAGTTTACTT	1020
CACAGGTAAA GACGGCTACG AAACAAAAGA CCTGACAGTT GAATGGGAAG AAGTTCCAGC	1080
GGAAAATCTG ACAAAGCAG GTCAATTTAC TGTTGAGGC CGTGTCTTG GTAGTAACCT	1140
TGTTGCTGAG ATCACTGTAC GAGTGACAGA CAACTTGGT GAGACTCTTT CAGATAACCC	1200
TAACATGAT GAAAACAGTA ACCAGGCCTT TGCTTCAGCA ACCAATGATA TTGACAAAA	1260
CTCTCATGAC CGCGTTGACT ATCTCAATGA CGGAGATCAT TCAGAAAATC GTCGTTGGAC	1320
AACTGGTCA CCAACACCAT CTTCTAATCC AGAAGTATCA GCGGGTGTGA TTTTCCGTGA	1380
AAATGGTAAG ATTGTAGAAC GGACTGTTAC ACAAGGAAAA GTTCAGTTCT TTGCAGATAG	1440
TGGTACGGAT GCACCATCTA AACTCGTTTT AGAACGCTAT GTCGGTCCAG AGTTTGAAAGT	1500
GCCAACCTAC TATTCAAACCT ACCAAGCCTA CGACGCAGAC CATCCATTCA ACAATCCAGA	1560
AAATTGGGAA GCTGTTCTTT ATCGTGCGGA TAAAGACATT GCAGCTGGTG ATGAAATCAA	1620
CGTAACATTT AAAGCTATCA AAGCCAAAGC TATGAGATGG CGTATGGAGC GTAAAGCAGA	1680
TAAGAGCGGT GTTGCGATGA TTGAGATGAC CTTCTTGCA CCAAGTGAAT TGCCTCAAGA	1740
AAGCACTCAA TCAAAGATTC TTGTAGATGG AAAAGAACTT GCTGATTTCG CTGAAAATCG	1800
TCAAGACTAT CAAATTACCT ATAAAGGTCA ACGGCCAAAA GTCTCAGTTG AAGAAAAACA	1860
TCAAGTAGCT TCAACTGTGG TAGATAGTGG AGAAGATAGC TTTCCAGTAC TTGTTGCGCT	1920
CGTTTCAGAA AGTGGAAC AAGTCAAGGA ATACCGTATC CACTTGACTA AGGAAAAACC	1980
AGTTTCTGAG AAGACAGTTG CTGCTGTACA AGAAGATCTT CCAAAAATCG AATTTGTTGA	2040
AAAAGATTTG GCATACAAGA CAGTTGAGAA AAAAGATTCA AACTGTATC TAGGTGAAAC	2100

TCGTGTAGAA CAAGAAGGAA AAGTTGGAAA AGAACGTATC TTTACAGCGA TTAATCCTGA 2160
 TGGAAGTAAG GAAGAAAAAC TCCGTGAAGT GGTAGAAGTT CCGACAGACC GCATCGTCTT 2220
 GGTGGAACC AAACAGTAG CTCAAGAAGC TAAAAACCA CAAGTGTCAG AAAAAGCAGA 2280
 TACAAAACCA ATTGATTCAA GTGAAGCTAG TCAAATAAT AAAGCCCAG 2329

(2) INFORMATION FOR SEQ ID NO:86:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 776 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:86:

Ala	Lys	Val	Ala	Trp	Asp	Ala	Ile	Arg	Pro	Glu	Gln	Tyr	Ala	Lys	Glu	1	5	10	15
Gly	Val	Phe	Thr	Val	Asn	Gly	Arg	Leu	Glu	Gly	Thr	Gln	Leu	Thr	Thr	20	25	30	
Lys	Leu	His	Val	Arg	Val	Ser	Ala	Gln	Thr	Glu	Gln	Gly	Ala	Asn	Ile	35	40	45	
Ser	Asp	Gln	Trp	Thr	Gly	Ser	Glu	Leu	Pro	Leu	Ala	Phe	Ala	Ser	Asp	50	55	60	
Ser	Asn	Pro	Ser	Asp	Pro	Val	Ser	Asn	Val	Asn	Asp	Lys	Leu	Ile	Ser	65	70	75	80
Tyr	Asn	Asn	Gln	Pro	Ala	Asn	Arg	Trp	Thr	Asn	Trp	Asn	Arg	Thr	Asn	85	90	95	
Pro	Glu	Ala	Ser	Val	Gly	Val	Leu	Phe	Gly	Asp	Ser	Gly	Ile	Leu	Ser	100	105	110	
Lys	Arg	Ser	Val	Asp	Asn	Leu	Ser	Val	Gly	Phe	His	Glu	Asp	His	Gly	115	120	125	
Val	Gly	Val	Pro	Lys	Ser	Tyr	Val	Ile	Glu	Tyr	Tyr	Val	Gly	Lys	Thr	130	135	140	
Val	Pro	Thr	Ala	Pro	Lys	Asn	Pro	Ser	Phe	Val	Gly	Asn	Glu	Asp	His	145	150	155	160
Val	Phe	Asn	Asp	Ser	Ala	Asn	Trp	Lys	Pro	Val	Thr	Asn	Leu	Lys	Ala	165	170	175	
Pro	Ala	Gln	Leu	Lys	Ala	Gly	Glu	Met	Asn	His	Phe	Ser	Phe	Asp	Lys	180	185	190	
Val	Glu	Thr	Tyr	Ala	Val	Arg	Ile	Arg	Met	Val	Lys	Ala	Asp	Asn	Lys	195	200	205	
Arg	Gly	Thr	Ser	Ile	Thr	Glu	Val	Gln	Ile	Phe	Ala	Lys	Gln	Val	Ala	210	215	220	

0076374 04200
 T0220 T229260

Ala Ala Lys Gln Gly Gln Thr Arg Ile Gln Val Asp Gly Lys Asp Leu
 225 230 235 240
 Ala Asn Phe Asn Pro Asp Leu Thr Asp Tyr Tyr Leu Glu Ser Val Asp
 245 250 255
 Gly Lys Val Pro Ala Val Thr Ala Ser Val Ser Asn Asn Gly Leu Ala
 260 265 270
 Thr Val Val Pro Ser Val Arg Glu Gly Glu Pro Val Arg Val Ile Ala
 275 280 285
 Lys Ala Glu Asn Gly Asp Ile Leu Gly Glu Tyr Arg Leu His Phe Thr
 290 295 300
 Lys Asp Lys Ser Leu Leu Ser His Lys Pro Val Ala Ala Val Lys Gln
 305 310 315 320
 Ala Arg Leu Leu Gln Val Gly Gln Ala Leu Glu Leu Pro Thr Lys Val
 325 330 335
 Pro Val Tyr Phe Thr Gly Lys Asp Gly Tyr Glu Thr Lys Asp Leu Thr
 340 345 350
 Val Glu Trp Glu Glu Val Pro Ala Glu Asn Leu Thr Lys Ala Gly Gln
 355 360 365
 Phe Thr Val Arg Gly Arg Val Leu Gly Ser Asn Leu Val Ala Glu Ile
 370 375 380
 Thr Val Arg Val Thr Asp Lys Leu Gly Glu Thr Leu Ser Asp Asn Pro
 385 390 395 400
 Asn Tyr Asp Glu Asn Ser Asn Gln Ala Phe Ala Ser Ala Thr Asn Asp
 405 410 415
 Ile Asp Lys Asn Ser His Asp Arg Val Asp Tyr Leu Asn Asp Gly Asp
 420 425 430
 His Ser Glu Asn Arg Arg Trp Thr Asn Trp Ser Pro Thr Pro Ser Ser
 435 440 445
 Asn Pro Glu Val Ser Ala Gly Val Ile Phe Arg Glu Asn Gly Lys Ile
 450 455 460
 Val Glu Arg Thr Val Thr Gln Gly Lys Val Gln Phe Phe Ala Asp Ser
 465 470 475 480
 Gly Thr Asp Ala Pro Ser Lys Leu Val Leu Glu Arg Tyr Val Gly Pro
 485 490 495
 Glu Phe Glu Val Pro Thr Tyr Tyr Ser Asn Tyr Gln Ala Tyr Asp Ala
 500 505 510
 Asp His Pro Phe Asn Asn Pro Glu Asn Trp Glu Ala Val Pro Tyr Arg
 515 520 525
 Ala Asp Lys Asp Ile Ala Ala Gly Asp Glu Ile Asn Val Thr Phe Lys
 530 535 540
 Ala Ile Lys Ala Lys Ala Met Arg Trp Arg Met Glu Arg Lys Ala Asp
 545 550 555 560

0076527-04204
 102210-1255100

Lys Ser Gly Val Ala Met Ile Glu Met Thr Phe Leu Ala Pro Ser Glu
565 570 575

Leu Pro Gln Glu Ser Thr Gln Ser Lys Ile Leu Val Asp Gly Lys Glu
580 585 590

Leu Ala Asp Phe Ala Glu Asn Arg Gln Asp Tyr Gln Ile Thr Tyr Lys
595 600 605

Gly Gln Arg Pro Lys Val Ser Val Glu Glu Asn Asn Gln Val Ala Ser
610 615 620

Thr Val Val Asp Ser Gly Glu Asp Ser Phe Pro Val Leu Val Arg Leu
625 630 635 640

Val Ser Glu Ser Gly Lys Gln Val Lys Glu Tyr Arg Ile His Leu Thr
645 650 655

Lys Glu Lys Pro Val Ser Glu Lys Thr Val Ala Ala Val Gln Glu Asp
660 665 670

Leu Pro Lys Ile Glu Phe Val Glu Lys Asp Leu Ala Tyr Lys Thr Val
675 680 685

Glu Lys Lys Asp Ser Thr Leu Tyr Leu Gly Glu Thr Arg Val Glu Gln
690 695 700

Glu Gly Lys Val Gly Lys Glu Arg Ile Phe Thr Ala Ile Asn Pro Asp
705 710 715 720

Gly Ser Lys Glu Glu Lys Leu Arg Glu Val Val Glu Val Pro Thr Asp
725 730 735

Arg Ile Val Leu Val Gly Thr Lys Pro Val Ala Gln Glu Ala Lys Lys
740 745 750

Pro Gln Val Ser Glu Lys Ala Asp Thr Lys Pro Ile Asp Ser Ser Glu
755 760 765

Ala Ser Gln Thr Asn Lys Ala Gln
770 775

(2) INFORMATION FOR SEQ ID NO: 87:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 133 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 87:

CTATCACTAT GTAAATAAAG AGATTATTTT ACAAGAAGCT AAAGATTTAA TTCAGACAGG	60
AAAGCCTGAC AGGAATGAAG TTGTATATGG TTTGGTGTAT CAAAAAGATC AGTTGCCTCA	120
AACAGGGACA GAA	133

(2) INFORMATION FOR SEQ ID NO: 88:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 44 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:88:

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Tyr His Tyr Val Asn Lys Glu Ile Ile Ser Gln Glu Ala Lys Asp Leu
1      5      10      15
Ile Gln Thr Gly Lys Pro Asp Arg Asn Glu Val Val Tyr Gly Leu Val
      20      25      30
Tyr Gln Lys Asp Gln Leu Pro Gln Thr Gly Thr Glu
      35      40

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(2) INFORMATION FOR SEQ ID NO: 89:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 775 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 89:

```

TGAGACTCCT CAATCAATAA CAAATCAGGA GCAAGCTAGG ACAGAAAACC AAGTAGTAGA      60
GACAGAGGAA GCTCCAAAAG AAGAAGCACC TAAACAGAA GAAAGTCCAA AGGAAGAACC      120
AAAATCGGAG GTAAACCTA CTGACGACAC CCTTCCTAAA GTAGAAGAGG GGAAAGAAGA      180
TTCAGCAGAA CCAGCTCCAG TTGAAGAAGT AGGTGGAGAA GTTGAGTCAA AACCAGAGGA      240
AAAAGTAGCA GTTAAGCCAG AAAGTCAACC ATCAGACAAA CCAGCTGAGG AATCAAAAGT      300
TGAACAAGCA GGTGAACCAG TCGCGCCAAG AGAAGACGAA AAGGCACCAG TCGAGCCAGA      360
AAAGCAACCA GAAGCTCCTG AAGAAGAGAA GGCTGTAGAG GAAACACCGA AACAAGAAGA      420
GTCAACTCCA GATACCAAGG CTGAAGAAAC TGTAGAACCA AAAGAGGAGA CTGTTAATCA      480
ATCTATTGAA CAACCAAAAG TTGAAACGCC TGCTGTAGAA AAACAAACAG AACCAACAGA      540
GGAACCAAAA GTTGAACAAG CAGGTGAACC AGTCGCGCCA AGAGAAGACG AACAGGCACC      600
AACGGCACCA GTTGAGCCAG AAAAGCAACC AGAAGTTCCT GAAGAAGAGA AGGCTGTAGA      660
GGAAACACCG AAACCAGAAG ATAAATAAAA GGGTATTGGT ACTAAAGAAC CAGTTGATAA      720
AAGTGAGTTA AATAATCAAA TTGATAAAGC TAGTTCAGTT TCTCCTACTG ATTAT      775

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(2) INFORMATION FOR SEQ ID NO:90:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 258 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:90:

Glu Thr Pro Gln Ser Ile Thr Asn Gln Glu Gln Ala Arg Thr Glu Asn
 1 5 10 15
 Gln Val Val Glu Thr Glu Glu Ala Pro Lys Glu Glu Ala Pro Lys Thr
 20 25 30
 Glu Glu Ser Pro Lys Glu Glu Pro Lys Ser Glu Val Lys Pro Thr Asp
 35 40 45
 Asp Thr Leu Pro Lys Val Glu Glu Gly Lys Glu Asp Ser Ala Glu Pro
 50 55 60
 Ala Pro Val Glu Glu Val Gly Gly Glu Val Glu Ser Lys Pro Glu Glu
 65 70 75 80
 Lys Val Ala Val Lys Pro Glu Ser Gln Pro Ser Asp Lys Pro Ala Glu
 85 90 95
 Glu Ser Lys Val Glu Gln Ala Gly Glu Pro Val Ala Pro Arg Glu Asp
 100 105 110
 Glu Lys Ala Pro Val Glu Pro Glu Lys Gln Pro Glu Ala Pro Glu Glu
 115 120 125
 Glu Lys Ala Val Glu Glu Thr Pro Lys Gln Glu Glu Ser Thr Pro Asp
 130 135 140
 Thr Lys Ala Glu Glu Thr Val Glu Pro Lys Glu Glu Thr Val Asn Gln
 145 150 155 160
 Ser Ile Glu Gln Pro Lys Val Glu Thr Pro Ala Val Glu Lys Gln Thr
 165 170 175
 Glu Pro Thr Glu Glu Pro Lys Val Glu Gln Ala Gly Glu Pro Val Ala
 180 185 190
 Pro Arg Glu Asp Glu Gln Ala Pro Thr Ala Pro Val Glu Pro Glu Lys
 195 200 205
 Gln Pro Glu Val Pro Glu Glu Glu Lys Ala Val Glu Glu Thr Pro Lys
 210 215 220
 Pro Glu Asp Lys Ile Lys Gly Ile Gly Thr Lys Glu Pro Val Asp Lys
 225 230 235 240
 Ser Glu Leu Asn Asn Gln Ile Asp Lys Ala Ser Ser Val Ser Pro Thr
 245 250 255
 Asp Tyr

(2) INFORMATION FOR SEQ ID NO: 91:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 199 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 91:

```

GGATGCTCAA GAAACTGCGG GAGTTCAC TA AATATGTG GCAGATTCAG AGCTATCATC      60
AGAAGAAAAG AAGCAGCTTG TCTATGATAT TCCGACATAC GTGGAGAATG ATGATGAAAC      120
TTATTATCTT GTTTATAAGT TAAATTCTCA AAATCAACTG GCGGAATTGC CAAATACTGG      180
AAGCAAGAAT GAGAGGCAA                                     199

```

(2) INFORMATION FOR SEQ ID NO:92:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 66 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:92:

```

Asp Ala Gln Glu Thr Ala Gly Val His Tyr Lys Tyr Val Ala Asp Ser
1           5           10           15
Glu Leu Ser Ser Glu Glu Lys Lys Gln Leu Val Tyr Asp Ile Pro Thr
          20           25           30
Tyr Val Glu Asn Asp Asp Glu Thr Tyr Tyr Leu Val Tyr Lys Leu Asn
          35           40           45
Ser Gln Asn Gln Leu Ala Glu Leu Pro Asn Thr Gly Ser Lys Asn Glu
          50           55           60
Arg Gln
65

```

(2) INFORMATION FOR SEQ ID NO: 93:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 835 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 93:

```

CGACAAAGGT GAGACTGAGG TTCAACCAGA GTCGCCAGAT ACTGTGGTAA GTGATAAAGG      60
TGAACCAGAG CAGGTAGCAC CGCTTCCAGA ATATAAGGGT AATATTGAGC AAGTAAAACC      120
TGAAACTCCG GTTGAGAAGA CCAAAGAACA AGGTCCAGAA AAAACTGAAG AAGTTCCAGT      180
AAAACCAACA GAAGAAACAC CAGTAAATCC AAATGAAGGT ACTACAGAAG GAACCTCAAT      240

```

TCAAGAAGCA GAAAATCCAG TTCAACCTGC AGAAGAATCA ACAACGAATT CAGAGAAAGT 300
 ATCACCAGAT ACATCTAGCA AAAATACTGG GGAAGTGTCC AGTAATCCTA GTGATTTCGAC 360
 AACCTCAGTT GGAGAATCAA ATAAACCAGA ACATAATGAC TCTAAAAATG AAAATTTCAGA 420
 AAAAAGTGTGA GAAGAAGTTC CAGTAAATCC AAATGAAGGC ACAGTAGAAG GTACCTCAAA 480
 TCAAGAAACA GAAAAACCAG TTCAACCTGC AGAAGAAACA CAAACAAACT CTGGGAAAAAT 540
 AGCTAACGAA AATACTGGAG AAGTATCCAA TAAACCTAGT GATTCAAAAC CACCAGTTGA 600
 AGAATCAAAT CAACCAGAAA AAAACGGAAC TGCAACAAAA CCAGAAAATT CAGGTAATAC 660
 AACATCAGAG AATGGACAAA CAGAACCAGA ACCATCAAAC GGAAATTCAA CTGAGGATGT 720
 TTCAACCGAA TCAAACACAT CCAATTCAAA TGGAAACGAA GAAATTAAAC AAGAAAAATGA 780
 ACTAGACCCT GATAAAAAGG TAGAAGAACC AGAGAAAACA CTTGAATTAA GAAAT 835

(2) INFORMATION FOR SEQ ID NO:94:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 278 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:94:

Asp Lys Gly Glu Thr Glu Val Gln Pro Glu Ser Pro Asp Thr Val Val
 1 5 10 15
 Ser Asp Lys Gly Glu Pro Glu Gln Val Ala Pro Leu Pro Glu Tyr Lys
 20 25 30
 Gly Asn Ile Glu Gln Val Lys Pro Glu Thr Pro Val Glu Lys Thr Lys
 35 40 45
 Glu Gln Gly Pro Glu Lys Thr Glu Glu Val Pro Val Lys Pro Thr Glu
 50 55 60
 Glu Thr Pro Val Asn Pro Asn Glu Gly Thr Thr Glu Gly Thr Ser Ile
 65 70 75 80
 Gln Glu Ala Glu Asn Pro Val Gln Pro Ala Glu Glu Ser Thr Thr Asn
 85 90 95
 Ser Glu Lys Val Ser Pro Asp Thr Ser Ser Lys Asn Thr Gly Glu Val
 100 105 110
 Ser Ser Asn Pro Ser Asp Ser Thr Thr Ser Val Gly Glu Ser Asn Lys
 115 120 125
 Pro Glu His Asn Asp Ser Lys Asn Glu Asn Ser Glu Lys Thr Val Glu
 130 135 140
 Glu Val Pro Val Asn Pro Asn Glu Gly Thr Val Glu Gly Thr Ser Asn
 145 150 155 160

Gln Glu Thr Glu Lys Pro Val Gln Pro Ala Glu Glu Thr Gln Thr Asn
 165 170 175

Ser Gly Lys Ile Ala Asn Glu Asn Thr Gly Glu Val Ser Asn Lys Pro
 180 185 190

Ser Asp Ser Lys Pro Pro Val Glu Glu Ser Asn Gln Pro Glu Lys Asn
 195 200 205

Gly Thr Ala Thr Lys Pro Glu Asn Ser Gly Asn Thr Thr Ser Glu Asn
 210 215 220

Gly Gln Thr Glu Pro Glu Pro Ser Asn Gly Asn Ser Thr Glu Asp Val
 225 230 235 240

Ser Thr Glu Ser Asn Thr Ser Asn Ser Asn Gly Asn Glu Glu Ile Lys
 245 250 255

Gln Glu Asn Glu Leu Asp Pro Asp Lys Lys Val Glu Glu Pro Glu Lys
 260 265 270

Thr Leu Glu Leu Arg Asn
 275

(2) INFORMATION FOR SEQ ID NO: 95:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 709 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 95:

AAATCAATTG GTAGCACAAG ATCCAAAAGC ACAAGATAGC ACTAAACTGA CTGCTGAAAA	60
ATCAACTGTT AAAGCACCTG CTCAAAGAGT AGATGTAAAA GATATAACTC ATTTAACAGA	120
TGAAGAAAAA GTTAAGGTTG CTATTTTACA AGCAAATGGT TCAGCATTAG ACGGAGCGAC	180
AATCAATGTA GCTGGAGATG GTACAGCAAC AATCACATTC CCAGATGGTT CAGTAGTGAC	240
GATTCTAGGA AAAGATACAG TTCAACAATC TGCGAAAGGT GAATCTGTAA CTCAAGAAGC	300
TACACCAGAG TATAAGCTAG AAAATACACC AGGTGGAGAT AAGGGAGGCA ATACTGGAAG	360
CTCAGATGCT AATGCGAATG AAGGCGGTGG TAGCCAGGCG GGTGGATCAG CTCACACAGG	420
TTACAAAAAC TCAGCTCAAT CACAAGCTTC TAAGCAATTA GCTACTGAAA AAGAATCAGC	480
TAAAAATGCC ATTGAAAAAG CAGCCAAGGA CAAGCAGGAT GAAATCAAAG GCGCACCGCT	540
TTCTGATAAA GAAAAAGCAG AACTTTTAGC AAGAGTGGAA GCAGAAAAAC AAGCAGCTCT	600
CAAAGAGATT GAAATGCGA AACTATGGA AGATGTGAAG GAAGCAGAAA CGATTGGAGT	660
GCAAGCCATT GCCATGGTTA CAGTTCCTAA GAGACCAGTG GCTCCTAAT	709

(2) INFORMATION FOR SEQ ID NO: 96:

(i) SEQUENCE CHARACTERISTICS:

(ii) MOLECULE.TYPE: protein

Asn	Gln	Leu	Val	Ala	Gln	Asp	Pro	Lys	Ala	Gln	Asp	Ser	Thr	Lys	Leu
1				5					10					15	
Thr	Ala	Glu	Lys	Ser	Thr	Val	Lys	Ala	Pro	Ala	Gln	Arg	Val	Asp	Val
		20					25						30		
Lys	Asp	Ile	Thr	His	Leu	Thr	Asp	Glu	Glu	Lys	Val	Lys	Val	Ala	Ile
		35					40					45			
Leu	Gln	Ala	Asn	Gly	Ser	Ala	Leu	Asp	Gly	Ala	Thr	Ile	Asn	Val	Ala
	50					55					60				
Gly	Asp	Gly	Thr	Ala	Thr	Ile	Thr	Phe	Pro	Asp	Gly	Ser	Val	Val	Thr
65					70					75					80
Ile	Leu	Gly	Lys	Asp	Thr	Val	Gln	Gln	Ser	Ala	Lys	Gly	Glu	Ser	Val
			85						90					95	
Thr	Gln	Glu	Ala	Thr	Pro	Glu	Tyr	Lys	Leu	Glu	Asn	Thr	Pro	Gly	Gly
			100					105					110		
Asp	Lys	Gly	Gly	Asn	Thr	Gly	Ser	Ser	Asp	Ala	Asn	Ala	Asn	Glu	Gly
		115					120					125			
Gly	Gly	Ser	Gln	Ala	Gly	Gly	Ser	Ala	His	Thr	Gly	Ser	Gln	Asn	Ser
	130					135					140				
Ala	Gln	Ser	Gln	Ala	Ser	Lys	Gln	Leu	Ala	Thr	Glu	Lys	Glu	Ser	Ala
145					150					155					160
Lys	Asn	Ala	Ile	Glu	Lys	Ala	Ala	Lys	Asp	Lys	Gln	Asp	Glu	Ile	Lys
			165						170					175	
Gly	Ala	Pro	Leu	Ser	Asp	Lys	Glu	Lys	Ala	Glu	Leu	Leu	Ala	Arg	Val
			180					185					190		
Glu	Ala	Glu	Lys	Gln	Ala	Ala	Leu	Lys	Glu	Ile	Glu	Asn	Ala	Lys	Thr
		195					200					205			
Met	Glu	Asp	Val	Lys	Glu	Ala	Glu	Thr	Ile	Gly	Val	Gln	Ala	Ile	Ala
	210					215					220				
Met	Val	Thr	Val	Pro	Lys	Arg	Pro	Val	Ala	Pro	Asn				
225					230					235					

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 787 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 97:

CAAACAGTCA GCTTCAGGAA CGATTGAGGT GATTTACGA GAAAATGGCT CTGGGACACG 60
GGGTGCCTTC ACAGAAATCA CAGGGATTCT CAAAAAGAC GGTGATAAAA AAATTGACAA 120
CACTGCCAAA ACAGCTGTGA TTCAAATAG TACAGAAGGT GTTCTCTCAG CAGTTCAAGG 180
GAATGCTAAT GCTATCGGCT ACATCTCCTT GGGATCTTTA ACGAAATCTG TCAAGGCTTT 240
AGAGATTGAT GGTGTCAAGG CTAGTCGAGA CACAGTTTTA GATGGTGAAT ACCCTCTTCA 300
ACGTCCCTTC AACATTGTTT GGTCTTCTAA TCTTTCCAAG CTAGGTCAAG ATTTTATCAG 360
CTTTATCCAC TCCAAACAAG GTCAACAAGT GGTCACAGAT AATAAATTTA TTGAAGCTAA 420
AACCGAACC ACGGAATATA CAAGCCAACA CTTATCAGGC AAGTTGTCTG TTGTAGGTTC 480
CACTTCAGTA TCTTCTTTAA TGGAAAAATT AGCAGAAGCT TATAAAAAAG AAAATCCAGA 540
AGTTACGATT GATATTACCT CTAATGGGTC TTCAGCAGGT ATTACCGCTG TTAAGGAGAA 600
AACCGCTGAT ATTGGTATGG TTTCTAGGGA ATTAACCTCT GAAGAAGGTA AGAGTCTCAC 660
CCATGATGCT ATTGCTTTAG ACGGTATTGC TGTTGTGGTC AATAATGACA ATAAGGCAAG 720
CCAAGTCAGT ATGGCTGAAC TTGCAGACGT TTTTAGTGGC AAATTAACCA CCTGGGACAA 780
GATTAAT 787

(2) INFORMATION FOR SEQ ID NO:98:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 262 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:98:

Lys Gln Ser Ala Ser Gly Thr Ile Glu Val Ile Ser Arg Glu Asn Gly
1 5 10 15
Ser Gly Thr Arg Gly Ala Phe Thr Glu Ile Thr Gly Ile Leu Lys Lys
20 25 30
Asp Gly Asp Lys Lys Ile Asp Asn Thr Ala Lys Thr Ala Val Ile Gln
35 40 45
Asn Ser Thr Glu Gly Val Leu Ser Ala Val Gln Gly Asn Ala Asn Ala
50 55 60
Ile Gly Tyr Ile Ser Leu Gly Ser Leu Thr Lys Ser Val Lys Ala Leu
65 70 75 80
Glu Ile Asp Gly Val Lys Ala Ser Arg Asp Thr Val Leu Asp Gly Glu
85 90 95

Tyr Pro Leu Gln Arg Pro Phe Asn Ile Val Trp Ser Ser Asn Leu Ser
 100 105 110
 Lys Leu Gly Gln Asp Phe Ile Ser Phe Ile His Ser Lys Gln Gly Gln
 115 120 125
 Gln Val Val Thr Asp Asn Lys Phe Ile Glu Ala Lys Thr Glu Thr Thr
 130 135 140
 Glu Tyr Thr Ser Gln His Leu Ser Gly Lys Leu Ser Val Val Gly Ser
 145 150 155 160
 Thr Ser Val Ser Ser Leu Met Glu Lys Leu Ala Glu Ala Tyr Lys Lys
 165 170 175
 Glu Asn Pro Glu Val Thr Ile Asp Ile Thr Ser Asn Gly Ser Ser Ala
 180 185 190
 Gly Ile Thr Ala Val Lys Glu Lys Thr Ala Asp Ile Gly Met Val Ser
 195 200 205
 Arg Glu Leu Thr Pro Glu Glu Gly Lys Ser Leu Thr His Asp Ala Ile
 210 215 220
 Ala Leu Asp Gly Ile Ala Val Val Val Asn Asn Asp Asn Lys Ala Ser
 225 230 235 240
 Gln Val Ser Met Ala Glu Leu Ala Asp Val Phe Ser Gly Lys Leu Thr
 245 250 255
 Thr Trp Asp Lys Ile Lys
 260

(2) INFORMATION FOR SEQ ID NO: 99:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 421 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 99:

ATTCGATGAT GCGGATGAAA AGATGACCCG TGATGAAATT GCCTATATGC TGACAAATAG 60
 TGAAGAAACA TTGGATGCTG ATGAGATTGA GATGCTACAA GGTGTCTTTT CGCTCGATGA 120
 ACTGATGGCA CGAGAGGTTA TGGTTCCTCG AACGGATGCC TTTATGGTGG ATATTCAGGA 180
 TGATAGTCAA GCCATTATCC AAAGTATTTT AAAACAAAAT TATTCTCGTA TCCCGGTTTA 240
 TGATGGGGAT AAGGACAATG TAATTGGAAT CATTACACCC AAGAGTCTCC TTAAGGCAGG 300
 CTTTGTGGAC GGTTTTGACA ATATTGTTTG GAAGAGAATT TTACAAGATC CACTTTTTGT 360
 ACCTGAAACT ATTTTGTGG ATGACTTGCT AAAAGAACTG CGAAATACCC AAAGACAAAT 420
 G 421

(2) INFORMATION FOR SEQ ID NO:100:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 140 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:100:

```

Phe Asp Asp Ala Asp Glu Lys Met Thr Arg Asp Glu Ile Ala Tyr Met
1      5      10      15
Leu Thr Asn Ser Glu Glu Thr Leu Asp Ala Asp Glu Ile Glu Met Leu
20     25     30
Gln Gly Val Phe Ser Leu Asp Glu Leu Met Ala Arg Glu Val Met Val
35     40     45
Pro Arg Thr Asp Ala Phe Met Val Asp Ile Gln Asp Asp Ser Gln Ala
50     55     60
Ile Ile Gln Ser Ile Leu Lys Gln Asn Tyr Ser Arg Ile Pro Val Tyr
65     70     75     80
Asp Gly Asp Lys Asp Asn Val Ile Gly Ile Ile His Thr Lys Ser Leu
85     90     95
Leu Lys Ala Gly Phe Val Asp Gly Phe Asp Asn Ile Val Trp Lys Arg
100    105    110
Ile Leu Gln Asp Pro Leu Phe Val Pro Glu Thr Ile Phe Val Asp Asp
115    120    125
Leu Leu Lys Glu Leu Arg Asn Thr Gln Arg Gln Met
130    135    140

```

(2) INFORMATION FOR SEQ ID NO: 101:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 331 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 101:

```

GGAGAGTCGA TCAAAAGTAG ATGAAGCTGT GTCTAAGTTT GAAAAGGACT CATCTTCTTC      60
GTCAAGTTCA GACTCTTCCA CTAAACCGGA AGCTTCAGAT ACAGCGAAGC CAAACAAGCC      120
GACAGAACCA GGAGAAAAGG TAGCAGAAGC TAAGAAGAAG GTTGAAGAAG CTGAGAAAAA      180
AGCCAAGGAT CAAAAGAAG AAGATCGTCG TAACTACCCA ACCATTACTT ACAAACGCT      240
TGAAGTTGAA ATTGCTGAGT CCGATGTGGA AGTTAAAAAA GCGGAGCTTG AACTAGTAAA      300
AGTGAAAGCT AACGAACCTC GAGACGAGCA A                                331

```

(2) INFORMATION FOR SEQ ID NO:102:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 110 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:102:

```

Glu Ser Arg Ser Lys Val Asp Glu Ala Val Ser Lys Phe Glu Lys Asp
1           5           10           15
Ser Ser Ser Ser Ser Ser Ser Asp Ser Ser Thr Lys Pro Glu Ala Ser
20           25           30
Asp Thr Ala Lys Pro Asn Lys Pro Thr Glu Pro Gly Glu Lys Val Ala
35           40           45
Glu Ala Lys Lys Lys Val Glu Glu Ala Glu Lys Lys Ala Lys Asp Gln
50           55           60
Lys Glu Glu Asp Arg Arg Asn Tyr Pro Thr Ile Thr Tyr Lys Thr Leu
65           70           75           80
Glu Leu Glu Ile Ala Glu Ser Asp Val Glu Val Lys Lys Ala Glu Leu
85           90           95
Glu Leu Val Lys Val Lys Ala Asn Glu Pro Arg Asp Glu Gln
100          105          110

```

(2) INFORMATION FOR SEQ ID NO: 103:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 358 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 103:

```

ATGGACAACA GGAAACTGGG ACGAGGTTAT ATCTGGTAAG ATTGACAAGT ACAAAGATCC      60
AGATATTCCA ACAGTTGAAT CACAAGAAGT TACGTCAGAC TCTAGTGATA AAGAAATAAC      120
GGTAAGGTAT GACCGTTTAT CAACACCAGA AAAACCAATC CCACAACCAA ATCCAGAGCA      180
TCCAAGTGTT CCGACACCAA ACCCAGAACT ACCAAATCAA GAGACTCCAA CACCAGATAA      240
ACCAACTCCA GAACCAGGTA CTCCAAAAAC TGAAACTCCA GTGAATCCAG ACCCAGAAGT      300
TCCGACTTAT GAGACAGGTA AGAGAGAGGA ATTGCCAAAC ACAGGTACAG AAGCTAAT      358

```

(2) INFORMATION FOR SEQ ID NO:104:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 119 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:104:

Trp Thr Thr Gly Asn Trp Asp Glu Val Ile Ser Gly Lys Ile Asp Lys
 1 5 10 15
 Tyr Lys Asp Pro Asp Ile Pro Thr Val Glu Ser Gln Glu Val Thr Ser
 20 25 30
 Asp Ser Ser Asp Lys Glu Ile Thr Val Arg Tyr Asp Arg Leu Ser Thr
 35 40 45
 Pro Glu Lys Pro Ile Pro Gln Pro Asn Pro Glu His Pro Ser Val Pro
 50 55 60
 Thr Pro Asn Pro Glu Leu Pro Asn Gln Glu Thr Pro Thr Pro Asp Lys
 65 70 75 80
 Pro Thr Pro Glu Pro Gly Thr Pro Lys Thr Glu Thr Pro Val Asn Pro
 85 90 95
 Asp Pro Glu Val Pro Thr Tyr Glu Thr Gly Lys Arg Glu Glu Leu Pro
 100 105 110
 Asn Thr Gly Thr Glu Ala Asn
 115

(2) INFORMATION FOR SEQ ID NO: 105:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1879 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 105:

CGATGGGCTC AATCCAACCC CAGGTCAAGT CTTACCTGAA GAGACATCGG GAACGAAAGA 60
 GGGTGACTTA TCAGAAAAAC CAGGAGACAC CGTTCTCACT CAAGCGAAAC CTGAGGGCGT 120
 TACTGGAAAT ACGAATTCAC TTCCGACACC TACAGAAAGA ACTGAAGTGA GCGAGGAAAC 180
 AAGCCCTTCT AGTCTGGATA CACTTTTTGA AAAAGATGAA GAAGCTCAAA AAAATCCAGA 240
 GCTAACAGAT GTCTTAAAG AAACTGTAGA TACAGCTGAT GTGGATGGGA CACAAGCAAG 300
 TCCAGCAGAA ACTACTCCTG AACAAGTAAA AGGTGGAGTG AAAGAAAATA CAAAAGACAG 360
 CATCGATGTT CCTGCTGCTT ATCTTGAAAA AGCTGAAGGG AAAGGTCCTT TCACTGCCGG 420
 TGTAACCAA GTAATTCCTT ATGAATATT CGCTGGTGAT GGTATGTTAA CTCGTCTATT 480
 ACTAAAAGCT TCGGATAATG CTCCTTGGTC TGACAATGGT ACTGCTAAAA ATCCTGCTTT 540
 ACCTCCTCTT GAAGGATTAA CAAAAGGGAA ATACTTCTAT GAAGTAGACT TAAATGGCAA 600

TACTGTTGGT AAACAAGGTC AAGCTTTAAT TGATCAACTT CGCGCTAATG GTACTCAAAC 660
 TTATAAAGCT ACTGTTAAAG TTTACGAAA TAAAGACGGT AAAGCTGACT TGACTAATCT 720
 AGTTGCTACT AAAAATGTAG ACATCAACAT CAATGGATTA GTTGCTAAAG AAACAGTTCA 780
 AAAAGCCGTT GCAGACAACG TTAAAGACAG TATCGATGTT CCAGCAGCCT ACCTAGAAAA 840
 AGCCAAGGGT GAAGGTCCAT TCACAGCAGG TGTCAACCAT GTGATTCCAT ACGAACTCTT 900
 CGCAGGTGAT GGCATGTTGA CTCGTCTCTT GCTCAAGGCA TCTGACAAGG CACCATGGTC 960
 AGATAACGGC GACGCTAAAA ACCCAGCCCT ATCTCCACTA GGCGAAAACG TGAAGACCAA 1020
 AGGTCAATAC TTCTATCAAN TAGCCTTGGA CGGAAATGTA GCTGGCAAAG AAAACAAGC 1080
 GCTCATTGAC CAGTTCCGAG CAAANGGTAC TCAAACCTAC AGCGCTACAG TCAATGTCTA 1140
 TGGTAACAAA GACGGTAAAC CAGACTTGGA CAACATCGTA GCAACTAAAA AAGTCACTAT 1200
 TAACATAAAC GGTTTAATTT CTAAAGAAAC AGTTCAAAAA GCCGTTGCAG ACAACGTTAA 1260
 NGACAGTATC GATGTTCCAG CAGCCTACCT AGAAAAAGCC AAGGGTGAAG GTCCATTAC 1320
 AGCAGGTGTC AACCATGTGA TTCCATACGA ACTCTTCGCA GGTGATGGTA TGTTGACTCG 1380
 TCTCTTGCTC AAGGCATCTG ACAAGGCACC ATGGTCAGAT AACGGNGACG CTA AAAACCC 1440
 AGCNCTATCT CCACTAGGTG AAAACGTGAA GACCAAAGGT CAATACTTCT ATCAANTAGC 1500
 CTTGGACGGA AATGTAGCTG GCAAAGAAAA ACAAGCGCTC ATTGACCAGT TCCGAGCAAA 1560
 CGGTACTCAA ACTTACAGCG CTACAGTCAA TGTCTATGGT AACAAAGACG GTAAACCAGA 1620
 CTTGGACAAC ATCGTAGCAA CTAAAAAGT CACTATTAAG ATAAATGTTA AAGAAACATC 1680
 AGACACAGCA AATGGTTCAT TATCACCTTC TAACTCTGGT TCTGGCGTGA CTCCGATGAA 1740
 TCACAATCAT GCTACAGGTA CTACAGATAG CATGCCTGCT GACACCATGA CAAGTTCTAC 1800
 CAACACGATG GCAGGTGAAA ACATGGCTGC TTCTGCTAAC AAGATGTCTG ATACGATGAT 1860
 GTCAGAGGAT AAAGCTATG 1879

(2) INFORMATION FOR SEQ ID NO:106:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 626 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:106:

Asp	Gly	Leu	Asn	Pro	Thr	Pro	Gly	Gln	Val	Leu	Pro	Glu	Glu	Thr	Ser
1				5				10				15			
Gly	Thr	Lys	Glu	Gly	Asp	Leu	Ser	Glu	Lys	Pro	Gly	Asp	Thr	Val	Leu
			20					25				30			

Thr Gln Ala Lys Pro Glu Gly Val Thr Gly Asn Thr Asn Ser Leu Pro
 35 40 45
 Thr Pro Thr Glu Arg Thr Glu Val Ser Glu Glu Thr Ser Pro Ser Ser
 50 55 60
 Leu Asp Thr Leu Phe Glu Lys Asp Glu Glu Ala Gln Lys Asn Pro Glu
 65 70 75 80
 Leu Thr Asp Val Leu Lys Glu Thr Val Asp Thr Ala Asp Val Asp Gly
 85 90 95
 Thr Gln Ala Ser Pro Ala Glu Thr Thr Pro Glu Gln Val Lys Gly Gly
 100 105 110
 Val Lys Glu Asn Thr Lys Asp Ser Ile Asp Val Pro Ala Ala Tyr Leu
 115 120 125
 Glu Lys Ala Glu Gly Lys Gly Pro Phe Thr Ala Gly Val Asn Gln Val
 130 135 140
 Ile Pro Tyr Glu Leu Phe Ala Gly Asp Gly Met Leu Thr Arg Leu Leu
 145 150 155 160
 Leu Lys Ala Ser Asp Asn Ala Pro Trp Ser Asp Asn Gly Thr Ala Lys
 165 170 175
 Asn Pro Ala Leu Pro Pro Leu Glu Gly Leu Thr Lys Gly Lys Tyr Phe
 180 185 190
 Tyr Glu Val Asp Leu Asn Gly Asn Thr Val Gly Lys Gln Gly Gln Ala
 195 200 205
 Leu Ile Asp Gln Leu Arg Ala Asn Gly Thr Gln Thr Tyr Lys Ala Thr
 210 215 220
 Val Lys Val Tyr Gly Asn Lys Asp Gly Lys Ala Asp Leu Thr Asn Leu
 225 230 235 240
 Val Ala Thr Lys Asn Val Asp Ile Asn Ile Asn Gly Leu Val Ala Lys
 245 250 255
 Glu Thr Val Gln Lys Ala Val Ala Asp Asn Val Lys Asp Ser Ile Asp
 260 265 270
 Val Pro Ala Ala Tyr Leu Glu Lys Ala Lys Gly Glu Gly Pro Phe Thr
 275 280 285
 Ala Gly Val Asn His Val Ile Pro Tyr Glu Leu Phe Ala Gly Asp Gly
 290 295 300
 Met Leu Thr Arg Leu Leu Leu Lys Ala Ser Asp Lys Ala Pro Trp Ser
 305 310 315 320
 Asp Asn Gly Asp Ala Lys Asn Pro Ala Leu Ser Pro Leu Gly Glu Asn
 325 330 335
 Val Lys Thr Lys Gly Gln Tyr Phe Tyr Gln Xaa Ala Leu Asp Gly Asn
 340 345 350
 Val Ala Gly Lys Glu Lys Gln Ala Leu Ile Asp Gln Phe Arg Ala Xaa
 355 360 365

Gly Thr Gln Thr Tyr Ser Ala Thr Val Asn Val Tyr Gly Asn Lys Asp
 370 375 380
 Gly Lys Pro Asp Leu Asp Asn Ile Val Ala Thr Lys Lys Val Thr Ile
 385 390 395 400
 Asn Ile Asn Gly Leu Ile Ser Lys Glu Thr Val Gln Lys Ala Val Ala
 405 410 415
 Asp Asn Val Xaa Asp Ser Ile Asp Val Pro Ala Ala Tyr Leu Glu Lys
 420 425 430
 Ala Lys Gly Glu Gly Pro Phe Thr Ala Gly Val Asn His Val Ile Pro
 435 440 445
 Tyr Glu Leu Phe Ala Gly Asp Gly Met Leu Thr Arg Leu Leu Leu Lys
 450 455 460
 Ala Ser Asp Lys Ala Pro Trp Ser Asp Asn Gly Asp Ala Lys Asn Pro
 465 470 475 480
 Ala Leu Ser Pro Leu Gly Glu Asn Val Lys Thr Lys Gly Gln Tyr Phe
 485 490 495
 Tyr Gln Xaa Ala Leu Asp Gly Asn Val Ala Gly Lys Glu Lys Gln Ala
 500 505 510
 Leu Ile Asp Gln Phe Arg Ala Asn Gly Thr Gln Thr Tyr Ser Ala Thr
 515 520 525
 Val Asn Val Tyr Gly Asn Lys Asp Gly Lys Pro Asp Leu Asp Asn Ile
 530 535 540
 Val Ala Thr Lys Lys Val Thr Ile Lys Ile Asn Val Lys Glu Thr Ser
 545 550 555 560
 Asp Thr Ala Asn Gly Ser Leu Ser Pro Ser Asn Ser Gly Ser Gly Val
 565 570 575
 Thr Pro Met Asn His Asn His Ala Thr Gly Thr Thr Asp Ser Met Pro
 580 585 590
 Ala Asp Thr Met Thr Ser Ser Thr Asn Thr Met Ala Gly Glu Asn Met
 595 600 605
 Ala Ala Ser Ala Asn Lys Met Ser Asp Thr Met Met Ser Glu Asp Lys
 610 615 620
 Ala Met
 625

(2) INFORMATION FOR SEQ ID NO: 107:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 593 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 107:

TTCCAATCAA AAACAGGCAG ATGGTAACT CAATATCGTG ACAACCTTTT ACCCTGTCTA 60
 TGA rTTTACC AAGCAAGTCG CAGGAGATAC GGCTAATGTA GAACTCCTAA TCGGTGCTGG 120
 GACAGAACCT CATGAATACG AACCATCTGC CAAGGCAGTT GCCAAAATCC AAGATGCAGA 180
 TACCTTCGTT TATGAAAATG AAAACATGGA AACATGGGTA CCTAAATTGC TAGATACCTT 240
 GGATAAGAAA AAAGTGAAAA CCATCAAGGC GACAGGCGAT ATGTTGCTCT TGCCAGGTGG 300
 CGAGGAAGAA GAGGGAGACC ATGACCATGG AGAAGAAGGT CATCACCATG AGTTTGACCC 360
 CCATGTTTGG TTATCACCAG TTCGTGCCAT tAAACTAGTA GAGCACCATC CGCGACACTT 420
 GTCAGCAGAT TATCCTGATA AAAAAGAGAC CTTTGAGAAG AATGCAGCTG CCTATATCGA 480
 AAAATTGCAA GCCTTGATA AGGCTTACGC AGAAGGTTTG TCTCAAGCAA AACAAAAGAG 540
 CTTTGTGACT CAACACGCAG CTTTAACTa TCTTGCCTTG GACTATGGGA CTC 593

(2) INFORMATION FOR SEQ ID NO:108:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 197 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:108:

Ser Asn Gln Lys Gln Ala Asp Gly Lys Leu Asn Ile Val Thr Thr Phe
 1 5 10 15
 Tyr Pro Val Tyr Glu Phe Thr Lys Gln Val Ala Gly Asp Thr Ala Asn
 20 25 30
 Val Glu Leu Leu Ile Gly Ala Gly Thr Glu Pro His Glu Tyr Glu Pro
 35 40 45
 Ser Ala Lys Ala Val Ala Lys Ile Gln Asp Ala Asp Thr Phe Val Tyr
 50 55 60
 Glu Asn Glu Asn Met Glu Thr Trp Val Pro Lys Leu Leu Asp Thr Leu
 65 70 75 80
 Asp Lys Lys Lys Val Lys Thr Ile Lys Ala Thr Gly Asp Met Leu Leu
 85 90 95
 Leu Pro Gly Gly Glu Glu Glu Glu Gly Asp His Asp His Gly Glu Glu
 100 105 110
 Gly His His His Glu Phe Asp Pro His Val Trp Leu Ser Pro Val Arg
 115 120 125
 Ala Ile Lys Leu Val Glu His His Pro Arg His Leu Ser Ala Asp Tyr
 130 135 140
 Pro Asp Lys Lys Glu Thr Phe Glu Lys Asn Ala Ala Ala Tyr Ile Glu
 145 150 155 160

Leu Asp Tyr Gly Thr
195

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1003 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 109:

TATCACAGGA	TCGAACGGTA	AGACAACCAC	AACGACTATG	ATTGGGGGAA	TTTGTACTGC	60
TGCTGGCCAA	CATGGTCTTT	TATCAGGGAA	TATCGGCTAT	CCAGCTAGTC	AGGTTGCTCA	120
AATAGCATCA	GATAAGGACA	CGCTTGTTAT	GGAACCTTCT	TCTTTCCAAC	TCATGGGTGT	180
TCAAGAATTC	CATCCAGAGA	TTGCGGTTAT	TACCAACCTC	ATGCCAACTC	ATATCGACTA	240
CCATGGGTCA	TTTTCGGAAT	ATGTAGCAGC	CAAGTGGAAT	ATCCAGAACA	AGATGACAGC	300
AGCTGATTTT	CTTGTCTTGA	ACTTTAATCA	AGACTTGGCA	AAAGACTTGA	CTTCCAAGAC	360
AGAAGCCACT	GTTGTACCAT	TTTCAACACT	TGAAAAGGTT	GATGGAGCTT	ATCTGGAAGA	420
TGGTCAACTC	TACTTCCGTG	GTGAAGTAGT	CATGGCAGCG	AATGAAATCG	GTGTTCCAGG	480
TAGCCACAAT	GTGGAAAATG	CCCTTGCGAC	TATTGCTGTA	GCCAAGCTTC	GTGATGTGGA	540
CAATCAAACC	ATCAAGGAAA	CTCTTTCAGC	CTTCGGTGGT	GTCAAACACC	GTCTCCAGTT	600
TGTGGATGAC	ATCAAGGGTG	TTAAATTCTA	TAACGACAGT	AAATCAACTA	ATATCTTGGC	660
TACTCAAAAA	GCCTTGTCAG	GATTTGACAA	CAGCAAGGTC	GTCTTGATTG	CAGGTGGTTT	720
GGACCGTGGC	AATGAGTTTG	ACGAATTGGT	GCCAGACATT	ACTGGACTCA	AGAAGATGGT	780
CATCCTGGGT	CAATCTGCAG	AACGTGTCAA	ACGGGCAGCA	GACAAGGCTG	GTGTCGCTTA	840
TGTGGAGGCG	ACAGATATTG	CAGATGCGAC	CCGCAAGGCC	TATGAGCTTG	CGACTCAAGG	900
AGATGTGGTT	CTTCTTAGTC	CTGCCAATGC	TAGCTGGGAT	ATGTATGCTA	ACTTTGAAGT	960
ACGTGGCGAC	CTCTTTATCG	ACACAGTAGC	GGAGTTAAAA	GAA		1003

(2) INFORMATION FOR SEQ ID NO:110:

- (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 335 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:110:

Gly Ile Thr Gly Ser Asn Gly Lys Thr Thr Thr Thr Thr Met Ile Gly
 1 5 10 15
 Glu Val Leu Thr Ala Ala Gly Gln His Gly Leu Leu Ser Gly Asn Ile
 20 25 30
 Gly Tyr Pro Ala Ser Gln Val Ala Gln Ile Ala Ser Asp Lys Asp Thr
 35 40 45
 Leu Val Met Glu Leu Ser Ser Phe Gln Leu Met Gly Val Gln Glu Phe
 50 55 60
 His Pro Glu Ile Ala Val Ile Thr Asn Leu Met Pro Thr His Ile Asp
 65 70 75 80
 Tyr His Gly Ser Phe Ser Glu Tyr Val Ala Ala Lys Trp Asn Ile Gln
 85 90 95
 Asn Lys Met Thr Ala Ala Asp Phe Leu Val Leu Asn Phe Asn Gln Asp
 100 105 110
 Leu Ala Lys Asp Leu Thr Ser Lys Thr Glu Ala Thr Val Val Pro Phe
 115 120 125
 Ser Thr Leu Glu Lys Val Asp Gly Ala Tyr Leu Glu Asp Gly Gln Leu
 130 135 140
 Tyr Phe Arg Gly Glu Val Val Met Ala Ala Asn Glu Ile Gly Val Pro
 145 150 155 160
 Gly Ser His Asn Val Glu Asn Ala Leu Ala Thr Ile Ala Val Ala Lys
 165 170 175
 Leu Arg Asp Val Asp Asn Gln Thr Ile Lys Glu Thr Leu Ser Ala Phe
 180 185 190
 Gly Gly Val Lys His Arg Leu Gln Phe Val Asp Asp Ile Lys Gly Val
 195 200 205
 Lys Phe Tyr Asn Asp Ser Lys Ser Thr Asn Ile Leu Ala Thr Gln Lys
 210 215 220
 Ala Leu Ser Gly Phe Asp Asn Ser Lys Val Val Leu Ile Ala Gly Gly
 225 230 235 240
 Leu Asp Arg Gly Asn Glu Phe Asp Glu Leu Val Pro Asp Ile Thr Gly
 245 250 255
 Leu Lys Lys Met Val Ile Leu Gly Gln Ser Ala Glu Arg Val Lys Arg
 260 265 270
 Ala Ala Asp Lys Ala Gly Val Ala Tyr Val Glu Ala Thr Asp Ile Ala
 275 280 285
 Asp Ala Thr Arg Lys Ala Tyr Glu Leu Ala Thr Gln Gly Asp Val Val
 290 295 300
 Leu Leu Ser Pro Ala Asn Ala Ser Trp Asp Met Tyr Ala Asn Phe Glu

305

310

315

320

Val Arg Gly Asp Leu Phe Ile Asp Thr Val Ala Glu Leu Lys Glu
 325 330 335

(2) INFORMATION FOR SEQ ID NO: 111:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 412 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 111:

AAGTTCATCG AAGATGGTTG GGAAGTCCAC TATATCGGGG ACAAGTGTGG TATCGAACAC 60
 CAAGAAATCC TTAAGTCAGG TTTGGATGTC ACCTTCCATT CTATTGCGAC TGGAAAATTG 120
 CGTCGCTATT TCTCTTGGCA AAATATGCTG GACGTCTTCA AAGTTGGTTG GGGAAATTGC 180
 CAATCGCTCT TTATCATGTT GCGACTGCGT CCACAGACCC TTTTTCAAA GGGGGGCTTT 240
 GTCTCAGTAC CGCCTGTTAT CGCTGCGCGT GTGTCAGGAG TGCCTGTCTT TATTCACGAA 300
 TCTGACCTGT CTATGGGCTT GGCCAATAAA ATCGCCTATA AATTTGCGAC TAAGATGTAT 360
 TCAACCTTTG AACAAGCTTC GAGTTTGGCT AAGGTTGAGC ATGTGGGAGC GG 412

(2) INFORMATION FOR SEQ ID NO:112:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 137 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:112:

Ser Ser Ser Lys Met Val Gly Lys Ser Thr Ile Ser Gly Thr Ser Val
 1 5 10 15
 Val Ser Asn Thr Lys Lys Ser Leu Ser Gln Val Trp Met Ser Pro Ser
 20 25 30
 Ile Leu Leu Arg Leu Glu Asn Cys Val Ala Ile Ser Leu Gly Lys Ile
 35 40 45
 Cys Trp Thr Ser Ser Lys Leu Val Gly Glu Leu Ser Asn Arg Ser Leu
 50 55 60
 Ser Cys Cys Asp Cys Val His Arg Pro Phe Phe Gln Arg Gly Ala Leu
 65 70 75 80
 Ser Gln Tyr Arg Leu Leu Ser Leu Arg Val Cys Gln Glu Cys Leu Ser
 85 90 95
 Leu Phe Thr Asn Leu Thr Cys Leu Trp Ala Trp Pro Ile Lys Ser Pro

100

105

110

Ile Asn Leu Arg Leu Arg Cys Ile Gln Pro Leu Asn Lys Leu Arg Val
 115 120 125

Trp Leu Arg Leu Ser Met Trp Glu Arg
 130 135

(2) INFORMATION FOR SEQ ID NO: 113:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 544 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 113:

ATCGCTAGCT AGTGAAATGC AAGAAAGTAC ACGTAAATTC AAGGTTACTG CTGACCTAAC 60
 AGATGCCGGT GTTGAACGA TTGAAGTTCC TTTGAGCATT GAAGATTTAC CCAATGGGCT 120
 GACCGCTGTG GCGACTCCGC AAAAAATTAC AGTCAAGATT GGTAAGAAGG CTCAGAAGGA 180
 TAAGGTAAAG ATTGTACCAG AGATTGACCC TAGTCAAATT GATAGTCGGG TACAAATTGA 240
 AAATGTCATG GTGTCAGATA AAGAAGTGTC TATTACGAGT GACCAAGAGA CATTGGATAG 300
 AATTGATAAG ATTATCGCTG TTTTGCCAAC TAGCGAACGT ATAACAGGTA ATTACAGTGG 360
 TTCAGTACCT TTGCAGGCAA TCGACCGCAA TGGTGTGTGTC TTACCGGCAG TTATCACTCC 420
 GTTTGATACA ATAATGAAGG TGACTIONAAA ACCAGTAGCA CCAAGTTCAA GCACATCAAA 480
 TTCAAGTACA AGCAGTTCAT CGGAGACATC TTCGTCAACG AAAGCAACTA GTTCAAAAAC 540
 GAAT 544

(2) INFORMATION FOR SEQ ID NO:114:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 181 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:114:

Ser Leu Ala Ser Glu Met Gln Glu Ser Thr Arg Lys Phe Lys Val Thr
 1 5 10 15

Ala Asp Leu Thr Asp Ala Gly Val Gly Thr Ile Glu Val Pro Leu Ser
 20 25 30

Ile Glu Asp Leu Pro Asn Gly Leu Thr Ala Val Ala Thr Pro Gln Lys
 35 40 45

Ile Thr Val Lys Ile Gly Lys Lys Ala Gln Lys Asp Lys Val Lys Ile

50	55	60
Val Pro Glu Ile Asp	Pro Ser Gln Ile Asp	Ser Arg Val Gln Ile Glu
65	70	75 80
Asn Val Met Val Ser	Asp Lys Glu Val Ser	Ile Thr Ser Asp Gln Glu
	85	90 95
Thr Leu Asp Arg Ile	Asp Lys Ile Ile Ala Val Leu	Pro Thr Ser Glu
	100	105 110
Arg Ile Thr Gly Asn	Tyr Ser Gly Ser Val Pro Leu	Gln Ala Ile Asp
	115	120 125
Arg Asn Gly Val Val	Leu Pro Ala Val Ile Thr	Pro Phe Asp Thr Ile
	130	135 140
Met Lys Val Thr Thr	Lys Pro Val Ala Pro Ser	Ser Ser Thr Ser Asn
	145	150 155 160
Ser Ser Thr Ser Ser	Ser Ser Glu Thr Ser	Ser Ser Thr Lys Ala Thr
	165	170 175
Ser Ser Lys Thr Asn		
	180	

(2) INFORMATION FOR SEQ ID NO: 115:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1267 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 115:

GCACCAGATG GGGCACAAGG TTCAGGGATC AGATGTTGAA AAGTACTACT TTACCCAACG	60
CGGTCTTGAG CAGGCAGGAA TTACCATTCT TCCTTTTGAT GAAAAAATC TAGACGGTGA	120
TATGGAAATT ATCGCTGGAA ATGCCTTTTCG TCCAGATAAC AACGTCGAAA TTGCCTATGC	180
GGACCAAAT GGTATCAGCT ACAAACGTTA CCATGAGTTT CTAGGTAGCT TTATGCGTGA	240
CTTTGTTAGC ATGGGAGTAG CAGGAGCACA TGGAAAACT TCAACGACAG GTATGTTGTC	300
TCATGTCTTG TCTCACATTA CAGATACCAG CTTCTTGATT GGAGATGGGA CAGGTCGTGG	360
TTCGGCCAAT GCCAAATATT TTGTCTTTGA ATCTGACGAA TATGAGCGTC ACTTCATGCC	420
TTACCACCCA GAATACTCTA TTATCACCAA CATTGACTTT GACCATCCAG ATTATTTTAC	480
AAGTCTCGAG GATGTTTTTA ATGCCTTTAA CGACTATGCC AAACAAATCA CCAAGGGTCT	540
TTTTGTCTAT GGTGAAGATG CTGAATTGCG TAAGATTACG TCTGATGCAC CAATTTATTA	600
TTATGGTTTT GAAGCTGAAG GCAATGACTT TGTAGCTAGT GATCTTCTTC GTTCAATAAC	660
TGGTTCAACC TTCACCGTTC ATTTCCGTGG ACAAACCTTG GGGCAATTCC ACATTCCAAC	720
CTTTGGTCGT CACAATATCA TGAATGCGAC AGCCGTTATT GGTCTTCTTT ACACAGCAGG	780

ATTTGATTTG AACTTGGTGC GTGAGCACTT GAAAACATTT GCCGGTGTTA AACGTCGTTT 840
 CACTGAGAAA ATTGTCAATG ATACAGTGAT TATCGATGAC TTTGCCCACC ATCCAACAGA 900
 AATTATTGCG ACCTTGGATG CGGCTCGTCA GAAATACCCA AGCAAGGAAA TTGTAGCAGT 960
 CTTTCAACCG CATACTTTA CAAGAACCAT TGCCTTGTTG GACGACTTTG CCCATGCTTT 1020
 AAACCAAGCA GATGCTGTTT ATCTAGCGCA AATTTATGGC TCGGCTCGTG AAGTAGATCA 1080
 TGGTGACGTT AAGGTAGAAG ACCTAGCCAA CAAAATCAAC AAAAAACACC AAGTGATTAC 1140
 TGTGAAAAT GTTTCTCCAC TCCTAGACCA TGACAATGCT GTTTACGTCT TTATGGGAGC 1200
 AGGAGACATC CAAACCTATG AATACTCATT TGAGCGTCTC TTGTCTAACT TGACAAGCAA 1260
 TGTTCAA 1267

(2) INFORMATION FOR SEQ ID NO:116:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 422 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:116:

His	Gln	Met	Gly	His	Lys	Val	Gln	Gly	Ser	Asp	Val	Glu	Lys	Tyr	Tyr	1	5	10	15
Phe	Thr	Gln	Arg	Gly	Leu	Glu	Gln	Ala	Gly	Ile	Thr	Ile	Leu	Pro	Phe	20	25	30	
Asp	Glu	Lys	Asn	Leu	Asp	Gly	Asp	Met	Glu	Ile	Ile	Ala	Gly	Asn	Ala	35	40	45	
Phe	Arg	Pro	Asp	Asn	Asn	Val	Glu	Ile	Ala	Tyr	Ala	Asp	Gln	Asn	Gly	50	55	60	
Ile	Ser	Tyr	Lys	Arg	Tyr	His	Glu	Phe	Leu	Gly	Ser	Phe	Met	Arg	Asp	65	70	75	80
Phe	Val	Ser	Met	Gly	Val	Ala	Gly	Ala	His	Gly	Lys	Thr	Ser	Thr	Thr	85	90	95	
Gly	Met	Leu	Ser	His	Val	Leu	Ser	His	Ile	Thr	Asp	Thr	Ser	Phe	Leu	100	105	110	
Ile	Gly	Asp	Gly	Thr	Gly	Arg	Gly	Ser	Ala	Asn	Ala	Lys	Tyr	Phe	Val	115	120	125	
Phe	Glu	Ser	Asp	Glu	Tyr	Glu	Arg	His	Phe	Met	Pro	Tyr	His	Pro	Glu	130	135	140	
Tyr	Ser	Ile	Ile	Thr	Asn	Ile	Asp	Phe	Asp	His	Pro	Asp	Tyr	Phe	Thr	145	150	155	160
Ser	Leu	Glu	Asp	Val	Phe	Asn	Ala	Phe	Asn	Asp	Tyr	Ala	Lys	Gln	Ile				

175

Leu Thr Ser Asn Val Gln
420

GGTTTCTAAA AGGGAAAATG GAAAGAAACG ACTTGTTTCAT TTTCTGCTGT TGA CTAGCAT 120
GGGAGTTCAA TTGTTGCCGG CCAGTGCTTT TGGGTTGACC AGCCAGATTT TATCTGCCTA 180
TAATAGTCAG CTTTCTATCG GAGTCGGGGA ACATTTACCA GAGCCTCTGA AAATCGAAGG 240
TTATCAATAT ATTGGTTATA TCAAAACTAA GAAACAGGAT AATACAGAGC TTTCAAGGAC 300
AGTTGATGGG AAATACTCTG CTCAAAGAGA TAGTCAACCA AACTCTACAA AAACATCAGA 360
TG TAGTTCAT TCAGCTGATT TAGAATGGAA CCAAGGACAG GGAAGGTTA GTTTACAAGG 420
TGAAGCATCA GGGGATGATG GACTTTTCAGA AAAATCTTCT ATAGCAGCAG ACAATCTATC 480
TTCTAATGAT TCATTCGCAA GTCAAGTTGA GCAGAATCCG GATCACAAAG GAGAATCTGT 540
AGTTGACCA ACAGTGCCAG AACAAGGAAA TCCTGTGTCT GCTACAACGG TGCAGAGTGC 600
GGAAGAGGAA GTATTGGCGA CGACAAATGA TCGACCAGAG TATAAACTTC CATTGGAAAC 660
CAAAGGCACG CAAGAACCCG GTCATGAGGG TGAAGCCGCA GTCCGTGAAG ACTTACCAGT 720
CTACACTAAG CCACTAGAAA CCAAAGGTAC ACAAGGACCC GGACATGAAG GTGAAGCTGC 780
AGTTGCGGAG GAAGAACCAG CTTACACAGA ACCGTTAGCA ACGAAAGGCA CGCAAGAGCC 840
AGGTCATGAG GGCAAAGCTA CAGTCCGCGA AGAGACTCTA GAGTACACGG AACC GG TAGC 900
GACAAAAGGC ACACAAGAAC CCGAACATGA GGGCGAaCGG SCAGTAGAAG AAGAACTTCC 960
GGCTTTAGAG GTC ACTACAC GAAATAGAAC GGAAATCCAG AATATTCCTT ATACAACAGA 1020
AGAAATTCAG GATCCAACAC TTCTGAAAAA TCGTCGTAAG ATTGAACGAC AAGGGCAAGC 1080
AGGGACACGT ACAATTCAAT ATGAAGACTA CATCGTAAAT GGTAATGTCTG TAGAACTAA 1140
AGAAGTGTCA CGAACTGAAG TAGCTCCGGT CAACGAAGTC GTTAAAGTAG GAACACTTGT 1200
GAAAGTTAAA CCTACAGTAG AAATTACAAA CTTAACAAAA GTTGAGAACA AAAAACTAT 1260
AACTGTAAGT TATAACTTAA TAGACACTAC CTCAGCATAT GTTTCTGCAA AAACGCAAGT 1320
TTTCCATGGA GACAAGCTAG TTAAAGAGGT GGATATAGAA AATCCTGCCA AAGAGCAAGT 1380
AATATCAGGT TTAGATTACT ACACACCGTA TACAGTTAAA ACACACCTAA CTTATAATTT 1440
GGGTGAAAAT AATGAGGAAA ATACTGAAAC ATCAACTCAA GATTTCCAAT TAGAGTATAA 1500
GAAAATAGAG ATTAAAGATA TTGATTCAGT AGAATTATAC GGTAAGAAA ATGATCGTTA 1560
TCGTAGATAT TTAAGTCTAA GTGAAGCGCC GACTGATACG GCTAAATACT TTGTAAAAGT 1620
GAAATCAGAT CGCTTCAAAG AAATGTACCT ACCTGTAAAA TCTATTACAG AAAATACGGA 1680
TGGAACGTAT AAAGTGACGG TAGCCGTTGA TCAACTTGTC GAAGAAGGTA CAGACGGTTA 1740
CAAAGATGAT TACACATTTA CTGTAGCTAA ATCTAAAGCA GAGCAACCAG GAGTTTACAC 1800
ATCCTTTAAA CAGCTGGTAA CAGCCATGCA AAGCAATCTG TCTGGTGTCT ATACATTGGC 1860
TTCAGATATG ACCGCAGATG AGGTGAGCTT AGGCGATAAG CAGACAAGTT ATCTCACAGG 1920

TGCATTTACA GGGAGCTTGA TCGGTTCTGA TGGAACAAAA TCGTATGCCA TTTATGATTT 1980
 GAAGAAACCA TTATTTGATA CATTAAATGG TGCTACAGTT AGAGATTTGG ATATTAAAC 2040
 TGTCTCTGCT GATAGTAAAG AAAATGTGCG AGCGCTGGCG AAGGCAGCGA ATAGCGCGAA 2100
 TATTAATAAT GTTGCAGTAG AAGGAAAAAT CTCAGGTGCG AAATCTGTTG CGGGATTAGT 2160
 AGCGAGCGCA ACAAATACAG TGATAGAAAA CAGCTCGTTT ACAGGGAAAC TTATCGCAAA 2220
 TCACCAGGAC AGTAATAAAA ATGATACTGG AGGAATAGTA GGTAATATAA CAGGAAATAG 2280
 TTCGAGAGTT AATAAAGTTA GGGTAGATGC CTTAATCTCT ACTAATGCAC GCAATAATAA 2340
 CCAAACAGCT GGAGGGATAG TAGGTAGATT AGAAAATGGT GCATTGATAT CTAATTCGGT 2400
 TGCTACTGGA GAAATACGAA ATGGTCAAGG ATATTCTAGA GTCGGAGGAA TAGTAGGATC 2460
 TACGTGGCAA AACGGTCGAG TAAATAATGT TGTGAGTAAC GTAGATGTTG GAGATGGTTA 2520
 TGTTATCACC GGTGATCAAT ACGCAGCAGC AGATGTGAAA AATGCAAGTA CATCAGTTGA 2580
 TAATAGAAAA GCAGACAGAT TCGCTACAAA ATTATCAAAA GACCAAATAG ACGCGAAAGT 2640
 TGCTGATTAT GGAATCACAG TAACTCTTGA TGATACTGGG CAAGATTTAA AACGTAATCT 2700
 AAGAGAAGTT GATTATACAA GACTAAATAA AGCAGAAGCT GAAAGAAAAG TAGCTTATAG 2760
 CAACATAGAA AAATGATGC CATTCTACAA TAAAGACCTA GTAGTTCATC ATGGTAACAA 2820
 AGTAGCGACA ACAGATAAAC TTTACACTAC AGAATTGTTA GATGTTGTGC CGATGAAAGA 2880
 TGATGAAGTA GTAACGGATA TTAATAATAA GAAAAATTCA ATAAATAAAG TTATGTTACA 2940
 TTTCAAAGAT AATACAGTAG AATACCTAGA TGTAACATTC AAAGAAAAC TCATAAACAG 3000
 TCAAGTAATC GAATACAATG TTACAGGAAA AGAATATATA TTCACACCAG AAGCATTTGT 3060
 TTCAGACTAT ACAGCGATAA CGAATAACGT ACTAAGCGAC TTGCAAAATG TAACACTTAA 3120
 C 3121

(2) INFORMATION FOR SEQ ID NO:118:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1040 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:118:

Phe Asn Pro Thr Val Gly Thr Phe Leu Phe Thr Ala Gly Leu Ser Leu
 1 5 10 15
 Leu Val Leu Leu Val Ser Lys Arg Glu Asn Gly Lys Lys Arg Leu Val
 20 25 30
 His Phe Leu Leu Thr Ser Met Gly Val Gln Leu Pro Ala Ser
 35 40 45

Ala Phe Gly Leu Thr Ser Gln Ile Leu Ser Ala Tyr Asn Ser Gln Leu
 50 55 60
 Ser Ile Gly Val Gly Glu His Leu Pro Glu Pro Leu Lys Ile Glu Gly
 65 70 75 80
 Tyr Gln Tyr Ile Gly Tyr Ile Lys Thr Lys Lys Gln Asp Asn Thr Glu
 85 90 95
 Leu Ser Arg Thr Val Asp Gly Lys Tyr Ser Ala Gln Arg Asp Ser Gln
 100 105 110
 Pro Asn Ser Thr Lys Thr Ser Asp Val Val His Ser Ala Asp Leu Glu
 115 120 125
 Trp Asn Gln Gly Gln Gly Lys Val Ser Leu Gln Gly Glu Ala Ser Gly
 130 135 140
 Asp Asp Gly Leu Ser Glu Lys Ser Ser Ile Ala Ala Asp Asn Leu Ser
 145 150 155 160
 Ser Asn Asp Ser Phe Ala Ser Gln Val Glu Gln Asn Pro Asp His Lys
 165 170 175
 Gly Glu Ser Val Val Arg Pro Thr Val Pro Glu Gln Gly Asn Pro Val
 180 185 190
 Ser Ala Thr Thr Val Gln Ser Ala Glu Glu Glu Val Leu Ala Thr Thr
 195 200 205
 Asn Asp Arg Pro Glu Tyr Lys Leu Pro Leu Glu Thr Lys Gly Thr Gln
 210 215 220
 Glu Pro Gly His Glu Gly Glu Ala Ala Val Arg Glu Asp Leu Pro Val
 225 230 235 240
 Tyr Thr Lys Pro Leu Glu Thr Lys Gly Thr Gln Gly Pro Gly His Glu
 245 250 255
 Gly Glu Ala Ala Val Arg Glu Glu Glu Pro Ala Tyr Thr Glu Pro Leu
 260 265 270
 Ala Thr Lys Gly Thr Gln Glu Pro Gly His Glu Gly Lys Ala Thr Val
 275 280 285
 Arg Glu Glu Thr Leu Glu Tyr Thr Glu Pro Val Ala Thr Lys Gly Thr
 290 295 300
 Gln Glu Pro Glu His Glu Gly Glu Arg Xaa Val Glu Glu Glu Leu Pro
 305 310 315 320
 Ala Leu Glu Val Thr Thr Arg Asn Arg Thr Glu Ile Gln Asn Ile Pro
 325 330 335
 Tyr Thr Thr Glu Glu Ile Gln Asp Pro Thr Leu Leu Lys Asn Arg Arg
 340 345 350
 Lys Ile Glu Arg Gln Gly Gln Ala Gly Thr Arg Thr Ile Gln Tyr Glu
 355 360 365
 Asp Tyr Ile Val Asn Gly Asn Val Val Glu Thr Lys Glu Val Ser Arg
 370 375 380

Thr Glu Val Ala Pro Val Asn Glu Val Val Lys Val Gly Thr Leu Val
 385 390 395 400
 Lys Val Lys Pro Thr Val Glu Ile Thr Asn Leu Thr Lys Val Glu Asn
 405 410 415
 Lys Lys Ser Ile Thr Val Ser Tyr Asn Leu Ile Asp Thr Thr Ser Ala
 420 425 430
 Tyr Val Ser Ala Lys Thr Gln Val Phe His Gly Asp Lys Leu Val Lys
 435 440 445
 Glu Val Asp Ile Glu Asn Pro Ala Lys Glu Gln Val Ile Ser Gly Leu
 450 455 460
 Asp Tyr Tyr Thr Pro Tyr Thr Val Lys Thr His Leu Thr Tyr Asn Leu
 465 470 475 480
 Gly Glu Asn Asn Glu Glu Asn Thr Glu Thr Ser Thr Gln Asp Phe Gln
 485 490 495
 Leu Glu Tyr Lys Lys Ile Glu Ile Lys Asp Ile Asp Ser Val Glu Leu
 500 505 510
 Tyr Gly Lys Glu Asn Asp Arg Tyr Arg Arg Tyr Leu Ser Leu Ser Glu
 515 520 525
 Ala Pro Thr Asp Thr Ala Lys Tyr Phe Val Lys Val Lys Ser Asp Arg
 530 535 540
 Phe Lys Glu Met Tyr Leu Pro Val Lys Ser Ile Thr Glu Asn Thr Asp
 545 550 555 560
 Gly Thr Tyr Lys Val Thr Val Ala Val Asp Gln Leu Val Glu Glu Gly
 565 570 575
 Thr Asp Gly Tyr Lys Asp Asp Tyr Thr Phe Thr Val Ala Lys Ser Lys
 580 585 590
 Ala Glu Gln Pro Gly Val Tyr Thr Ser Phe Lys Gln Leu Val Thr Ala
 595 600 605
 Met Gln Ser Asn Leu Ser Gly Val Tyr Thr Leu Ala Ser Asp Met Thr
 610 615 620
 Ala Asp Glu Val Ser Leu Gly Asp Lys Gln Thr Ser Tyr Leu Thr Gly
 625 630 635 640
 Ala Phe Thr Gly Ser Leu Ile Gly Ser Asp Gly Thr Lys Ser Tyr Ala
 645 650 655
 Ile Tyr Asp Leu Lys Lys Pro Leu Phe Asp Thr Leu Asn Gly Ala Thr
 660 665 670
 Val Arg Asp Leu Asp Ile Lys Thr Val Ser Ala Asp Ser Lys Glu Asn
 675 680 685
 Val Ala Ala Leu Ala Lys Ala Ala Asn Ser Ala Asn Ile Asn Asn Val
 690 695 700
 Ala Val Glu Gly Lys Ile Ser Gly Ala Lys Ser Val Ala Gly Leu Val
 705 710 715 720

0976324 043304
T00040 12099260

Ala Ser Ala Thr Asn Thr Val Ile Glu Asn Ser Ser Phe Thr Gly Lys
 725 730 735
 Leu Ile Ala Asn His Gln Asp Ser Asn Lys Asn Asp Thr Gly Gly Ile
 740 745 750
 Val Gly Asn Ile Thr Gly Asn Ser Ser Arg Val Asn Lys Val Arg Val
 755 760 765
 Asp Ala Leu Ile Ser Thr Asn Ala Arg Asn Asn Asn Gln Thr Ala Gly
 770 775 780
 Gly Ile Val Gly Arg Leu Glu Asn Gly Ala Leu Ile Ser Asn Ser Val
 785 790 795 800
 Ala Thr Gly Glu Ile Arg Asn Gly Gln Gly Tyr Ser Arg Val Gly Gly
 805 810 815
 Ile Val Gly Ser Thr Trp Gln Asn Gly Arg Val Asn Asn Val Val Ser
 820 825 830
 Asn Val Asp Val Gly Asp Gly Tyr Val Ile Thr Gly Asp Gln Tyr Ala
 835 840 845
 Ala Ala Asp Val Lys Asn Ala Ser Thr Ser Val Asp Asn Arg Lys Ala
 850 855 860
 Asp Arg Phe Ala Thr Lys Leu Ser Lys Asp Gln Ile Asp Ala Lys Val
 865 870 875 880
 Ala Asp Tyr Gly Ile Thr Val Thr Leu Asp Asp Thr Gly Gln Asp Leu
 885 890 895
 Lys Arg Asn Leu Arg Glu Val Asp Tyr Thr Arg Leu Asn Lys Ala Glu
 900 905 910
 Ala Glu Arg Lys Val Ala Tyr Ser Asn Ile Glu Lys Leu Met Pro Phe
 915 920 925
 Tyr Asn Lys Asp Leu Val Val His Tyr Gly Asn Lys Val Ala Thr Thr
 930 935 940
 Asp Lys Leu Tyr Thr Thr Glu Leu Leu Asp Val Val Pro Met Lys Asp
 945 950 955 960
 Asp Glu Val Val Thr Asp Ile Asn Asn Lys Lys Asn Ser Ile Asn Lys
 965 970 975
 Val Met Leu His Phe Lys Asp Asn Thr Val Glu Tyr Leu Asp Val Thr
 980 985 990
 Phe Lys Glu Asn Phe Ile Asn Ser Gln Val Ile Glu Tyr Asn Val Thr
 995 1000 1005
 Gly Lys Glu Tyr Ile Phe Thr Pro Glu Ala Phe Val Ser Asp Tyr Thr
 1010 1015 1020
 Ala Ile Thr Asn Asn Val Leu Ser Asp Leu Gln Asn Val Thr Leu Asn
 1025 1030 1035 1040

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1567 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 119:

TTTTAACCCA	ACTGTTGGTA	CTTTCCTTTT	TACTGCAGGA	TTGAGCTTGT	TAGTTTTATT	60
GGTTTCTAAA	AGGGAAAATG	GAAAGAAACG	ACTTGTTTCAT	TTTCTGCTGT	TGACTAGCAT	120
GGGAGTTCAA	TTGTTGCCGG	CCAGTGCTTT	TGGGTTGACC	AGCCAGATTT	TATCTGCCTA	180
TAATAGTCAG	CTTTCATCG	GAGTCGGGGA	ACATTTACCA	GAGCCTCTGA	AAATCGAAGG	240
TTATCAATAT	ATTGGTTATA	TCAAAACTAA	GAAACAGGAT	AATACAGAGC	TTTCAAGGAC	300
AGTTGATGGG	AAATACTCTG	CTCAAAGAGA	TAGTCAACCA	AACTCTACAA	AAACATCAGA	360
TGTAGTTCAT	TCAGCTGATT	TAGAATGGAA	CCAAGGACAG	GGGAAGGTTA	GTTTACAAGG	420
TGAAGCATCA	GGGGATGATG	GACTTTTCAGA	AAAATCTTCT	ATAGCAGCAG	ACAATCTATC	480
TTCTAATGAT	TCATTCGCAA	GTCAAGTTGA	GCAGAATCCG	GATCACAAAG	GAGAATCTGT	540
AGTTTCGACCA	ACAGTGCCAG	AACAAGGAAA	TCCTGTGTCT	GCTACAACGG	TGCAGAGTGC	600
GGAAGAGGAA	GTATTGGCGA	CGACAAATGA	TCGACCAGAG	TATAAACTTC	CATTGGAAAC	660
CAAAGGCACG	CAAGAACCCG	GTCATGAGGG	TGAAGCCGCA	GTCCGTGAAG	ACTTACCAGT	720
CTACACTAAG	CCACTAGAAA	CCAAAGGTAC	ACAAGGACCC	GGACATGAAG	GTGAAGCTGC	780
AGTTTCGCGAG	GAAGAACCAG	CTTACACAGA	ACCGTTAGCA	ACGAAAGGCA	CGCAAGAGCC	840
AGGTCATGAG	GGCAAAGCTA	CAGTCCGCGA	AGAGACTCTA	GAGTACACGG	AACCGGTAGC	900
GACAAAAGGC	ACACAAGAAC	CCGAACATGA	GGGCGAaCGG	scAGTAGAAG	AAGAACTTCC	960
GGCTTTAGAG	GTCACTACAC	GAAATAGAAC	GGAAATCCAG	AATATTCCCTT	ATACAACAGA	1020
AGAAATTCAG	GATCCAACAC	TTCTGAAAAA	TCGTCGTAAG	ATTGAACGAC	AAGGGCAAGC	1080
AGGGACACGT	ACAATTCAAT	ATGAAGACTA	CATCGTAAAT	GGTAATGTCTG	TAGAAACTAA	1140
AGAAGTGTC	CGAACTGAAG	TAGCTCCGGT	CAACGAAGTC	GTTAAAGTAG	GAACACTTGT	1200
GAAAGTTAAA	CCTACAGTAG	AAATTACAAA	CTTAACAAAA	GTTGAGAACA	AAAAATCTAT	1260
AACTGTAAGT	TATAACTTAA	TAGACACTAC	CTCAGCATAT	GTTTCTGCAA	AAACGCAAGT	1320
TTTCCATGGA	GACAAGCTAG	TTAAAGAGGT	GGATATAGAA	AATCCTGCCA	AAGAGCAAGT	1380
AATATCAGGT	TTAGATTACT	ACACACCGTA	TACAGTTAAA	ACACACCTAA	CTTATAATTT	1440
GGGTGAAAAT	AATGAGGAAA	ATACTGAAAC	ATCAACTCAA	GATTTCCAAT	TAGAGTATAA	1500
GAAAATAGAG	ATTAAAGATA	TTGATTCAGT	AGAATTATAC	GGTAAAGAAA	ATGATCGTTA	1560
TCGTAGA						1567

(2) INFORMATION FOR SEQ ID NO:120:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 522 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:120:

Phe	Asn	Pro	Thr	Val	Gly	Thr	Phe	Leu	Phe	Thr	Ala	Gly	Leu	Ser	Leu	1	5	10	15
Leu	Val	Leu	Leu	Val	Ser	Lys	Arg	Glu	Asn	Gly	Lys	Lys	Arg	Leu	Val	20	25	30	
His	Phe	Leu	Leu	Leu	Thr	Ser	Met	Gly	Val	Gln	Leu	Leu	Pro	Ala	Ser	35	40	45	
Ala	Phe	Gly	Leu	Thr	Ser	Gln	Ile	Leu	Ser	Ala	Tyr	Asn	Ser	Gln	Leu	50	55	60	
Ser	Ile	Gly	Val	Gly	Glu	His	Leu	Pro	Glu	Pro	Leu	Lys	Ile	Glu	Gly	65	70	75	80
Tyr	Gln	Tyr	Ile	Gly	Tyr	Ile	Lys	Thr	Lys	Lys	Gln	Asp	Asn	Thr	Glu	85	90	95	
Leu	Ser	Arg	Thr	Val	Asp	Gly	Lys	Tyr	Ser	Ala	Gln	Arg	Asp	Ser	Gln	100	105	110	
Pro	Asn	Ser	Thr	Lys	Thr	Ser	Asp	Val	Val	His	Ser	Ala	Asp	Leu	Glu	115	120	125	
Trp	Asn	Gln	Gly	Gln	Gly	Lys	Val	Ser	Leu	Gln	Gly	Glu	Ala	Ser	Gly	130	135	140	
Asp	Asp	Gly	Leu	Ser	Glu	Lys	Ser	Ser	Ile	Ala	Ala	Asp	Asn	Leu	Ser	145	150	155	160
Ser	Asn	Asp	Ser	Phe	Ala	Ser	Gln	Val	Glu	Gln	Asn	Pro	Asp	His	Lys	165	170	175	
Gly	Glu	Ser	Val	Val	Arg	Pro	Thr	Val	Pro	Glu	Gln	Gly	Asn	Pro	Val	180	185	190	
Ser	Ala	Thr	Thr	Val	Gln	Ser	Ala	Glu	Glu	Glu	Val	Leu	Ala	Thr	Thr	195	200	205	
Asn	Asp	Arg	Pro	Glu	Tyr	Lys	Leu	Pro	Leu	Glu	Thr	Lys	Gly	Thr	Gln	210	215	220	
Glu	Pro	Gly	His	Glu	Gly	Glu	Ala	Ala	Val	Arg	Glu	Asp	Leu	Pro	Val	225	230	235	240
Tyr	Thr	Lys	Pro	Leu	Glu	Thr	Lys	Gly	Thr	Gln	Gly	Pro	Gly	His	Glu	245	250	255	
Gly	Glu	Ala	Ala	Val	Arg	Glu	Glu	Glu	Pro	Ala	Tyr	Thr	Glu	Pro	Leu				

236

260

265

270

Ala Thr Lys Gly Thr Gln Glu Pro Gly His Glu Gly Lys Ala Thr Val
275 280 285

Arg Glu Glu Thr Leu Glu Tyr Thr Glu Pro Val Ala Thr Lys Gly Thr
290 295 300

Gln Glu Pro Glu His Glu Gly Glu Arg Xaa Val Glu Glu Glu Leu Pro
305 310 315 320

Ala Leu Glu Val Thr Thr Arg Asn Arg Thr Glu Ile Gln Asn Ile Pro
325 330 335

Tyr Thr Thr Glu Glu Ile Gln Asp Pro Thr Leu Leu Lys Asn Arg Arg
340 345 350

Lys Ile Glu Arg Gln Gly Gln Ala Gly Thr Arg Thr Ile Gln Tyr Glu
355 360 365

Asp Tyr Ile Val Asn Gly Asn Val Val Glu Thr Lys Glu Val Ser Arg
370 375 380

Thr Glu Val Ala Pro Val Asn Glu Val Val Lys Val Gly Thr Leu Val
385 390 395 400

Lys Val Lys Pro Thr Val Glu Ile Thr Asn Leu Thr Lys Val Glu Asn
405 410 415

Lys Lys Ser Ile Thr Val Ser Tyr Asn Leu Ile Asp Thr Thr Ser Ala
420 425 430

Tyr Val Ser Ala Lys Thr Gln Val Phe His Gly Asp Lys Leu Val Lys
435 440 445

Glu Val Asp Ile Glu Asn Pro Ala Lys Glu Gln Val Ile Ser Gly Leu
450 455 460

Asp Tyr Tyr Thr Pro Tyr Thr Val Lys Thr His Leu Thr Tyr Asn Leu
465 470 475 480

Gly Glu Asn Asn Glu Glu Asn Thr Glu Thr Ser Thr Gln Asp Phe Gln
485 490 495

Leu Glu Tyr Lys Lys Ile Glu Ile Lys Asp Ile Asp Ser Val Glu Leu
500 505 510

Tyr Gly Lys Glu Asn Asp Arg Tyr Arg Arg
515 520

(2) INFORMATION FOR SEQ ID NO: 121:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1561 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 121:

TCGTAGATAT TTAAGTCTAA GTGAAGCGCC GACTGATACG GCTAAATACT TTGTAAAAGT

GAAATCAGAT CGCTTCAAAG AAATGTACCT ACCTGTAAAA TCTATTACAG AAAATACGGA 120
 TGGAACGTAT AAAGTGACGG TAGCCGTTGA TCAACTTGTC GAAGAAGGTA CAGACGGTTA 180
 CAAAGATGAT TACACATTTA CTGTAGCTAA ATCTAAAGCA GAGCAACCAG GAGTTTACAC 240
 ATCCTTTAAA CAGCTGGTAA CAGCCATGCA AAGCAATCTG TCTGGTGTCT ATACATTGGC 300
 TTCAGATATG ACCGCAGATG AGGTGAGCTT AGGCGATAAG CAGACAAGTT ATCTCACAGG 360
 TGCATTTACA GGGAGCTTGA TCGGTTCTGA TGGAACAAAA TCGTATGCCA TTTATGATTT 420
 GAAGAAACCA TTATTTGATA CATTAAATGG TGCTACAGTT AGAGATTTGG ATATTAAAC 480
 TGTTCCTGCT GATAGTAAAG AAAATGTCGC AGCGCTGGCG AAGGCAGCGA ATAGCGCGAA 540
 TATTAATAAT GTTGCAGTAG AAGGAAAAAT CTCAGGTGCG AAATCTGTTG CGGGATTAGT 600
 AGCGAGCGCA ACAATAACAG TGATAGAAAA CAGCTCGTTT ACAGGGAAAC TTATCGCAAA 660
 TCACCAGGAC AGTAATAAAA ATGATACTGG AGGAATAGTA GGTAATATAA CAGGAAATAG 720
 TTCGAGAGTT AATAAAGTTA GGGTAGATGC CTTAATCTCT ACTAATGCAC GCAATAATAA 780
 CCAAACAGCT GGAGGGATAG TAGGTAGATT AGAAAATGGT GCATTGATAT CTAATTCGGT 840
 TGCTACTGGA GAAATACGAA ATGGTCAAGG ATATTCTAGA GTCGGAGGAA TAGTAGGATC 900
 TACGTGGCAA AACGGTCGAG TAAATAATGT TGTGAGTAAC GTAGATGTTG GAGATGGTTA 960
 TGTTATCACC GGTGATCAAT ACGCAGCAGC AGATGTGAAA AATGCAAGTA CATCAGTTGA 1020
 TAATAGAAAA GCAGACAGAT TCGCTACAAA ATTATCAAAA GACCAAATAG ACGCGAAAGT 1080
 TGCTGATTAT GGAATCACAG TAACTCTTGA TGATACTGGG CAAGATTTAA AACGTAATCT 1140
 AAGAGAAGTT GATTATACAA GACTAAATAA AGCAGAAGCT GAAAGAAAAG TAGCTTATAG 1200
 CAACATAGAA AACTGATGC CATTCTACAA TAAAGACCTA GTAGTTCACCT ATGGTAACAA 1260
 AGTAGCGACA ACAGATAAAC TTTACACTAC AGAATTGTGA GATGTTGTGC CGATGAAAGA 1320
 TGATGAAGTA GTAACGGATA TTAATAATAA GAAAAATTCA ATAAATAAAG TTATGTTACA 1380
 TTTCAAAGAT AATACAGTAG AATACCTAGA TGTAACATTC AAAGAAAAC TCATAAACAG 1440
 TCAAGTAATC GAATACAATG TTACAGGAAA AGAATATATA TTCACACCAG AAGCATTTGT 1500
 TTCAGACTAT ACAGCGATAA CGAATAACGT ACTAAGCGAC TTGCAAAATG TAACACTTAA 1560
 C 1561

(2) INFORMATION FOR SEQ ID NO:122:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 520 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

Arg	Arg	Tyr	Leu	Ser	Leu	Ser	Glu	Ala	Pro	Thr	Asp	Thr	Ala	Lys	Tyr
1				5					10					15	
Phe	Val	Lys	Val	Lys	Ser	Asp	Arg	Phe	Lys	Glu	Met	Tyr	Leu	Pro	Val
			20					25					30		
Lys	Ser	Ile	Thr	Glu	Asn	Thr	Asp	Gly	Thr	Tyr	Lys	Val	Thr	Val	Ala
		35					40					45			
Val	Asp	Gln	Leu	Val	Glu	Glu	Gly	Thr	Asp	Gly	Tyr	Lys	Asp	Asp	Tyr
	50					55					60				
Thr	Phe	Thr	Val	Ala	Lys	Ser	Lys	Ala	Glu	Gln	Pro	Gly	Val	Tyr	Thr
65					70					75					80
Ser	Phe	Lys	Gln	Leu	Val	Thr	Ala	Met	Gln	Ser	Asn	Leu	Ser	Gly	Val
				85					90					95	
Tyr	Thr	Leu	Ala	Ser	Asp	Met	Thr	Ala	Asp	Glu	Val	Ser	Leu	Gly	Asp
			100					105					110		
Lys	Gln	Thr	Ser	Tyr	Leu	Thr	Gly	Ala	Phe	Thr	Gly	Ser	Leu	Ile	Gly
		115					120					125			
Ser	Asp	Gly	Thr	Lys	Ser	Tyr	Ala	Ile	Tyr	Asp	Leu	Lys	Lys	Pro	Leu
	130					135					140				
Phe	Asp	Thr	Leu	Asn	Gly	Ala	Thr	Val	Arg	Asp	Leu	Asp	Ile	Lys	Thr
145					150					155					160
Val	Ser	Ala	Asp	Ser	Lys	Glu	Asn	Val	Ala	Ala	Leu	Ala	Lys	Ala	Ala
				165					170					175	
Asn	Ser	Ala	Asn	Ile	Asn	Asn	Val	Ala	Val	Glu	Gly	Lys	Ile	Ser	Gly
			180					185					190		
Ala	Lys	Ser	Val	Ala	Gly	Leu	Val	Ala	Ser	Ala	Thr	Asn	Thr	Val	Ile
		195					200					205			
Glu	Asn	Ser	Ser	Phe	Thr	Gly	Lys	Leu	Ile	Ala	Asn	His	Gln	Asp	Ser
	210					215					220				
Asn	Lys	Asn	Asp	Thr	Gly	Gly	Ile	Val	Gly	Asn	Ile	Thr	Gly	Asn	Ser
225					230					235					240
Ser	Arg	Val	Asn	Lys	Val	Arg	Val	Asp	Ala	Leu	Ile	Ser	Thr	Asn	Ala
				245					250					255	
Arg	Asn	Asn	Asn	Gln	Thr	Ala	Gly	Gly	Ile	Val	Gly	Arg	Leu	Glu	Asn
			260					265					270		
Gly	Ala	Leu	Ile	Ser	Asn	Ser	Val	Ala	Thr	Gly	Glu	Ile	Arg	Asn	Gly
		275					280					285			
Gln	Gly	Tyr	Ser	Arg	Val	Gly	Gly	Ile	Val	Gly	Ser	Thr	Trp	Gln	Asn
	290					295					300				
Gly	Arg	Val	Asn	Asn	Val	Val	Ser	Asn	Val	Asp	Val	Gly	Asp	Gly	Tyr
305					310					315					320

Val Ile Thr Gly Asp Gln Tyr Ala Ala Asp Val Lys Asn Ala Ser
 325 330 335
 Thr Ser Val Asp Asn Arg Lys Ala Asp Arg Phe Ala Thr Lys Leu Ser
 340 345 350
 Lys Asp Gln Ile Asp Ala Lys Val Ala Asp Tyr Gly Ile Thr Val Thr
 355 360 365
 Leu Asp Asp Thr Gly Gln Asp Leu Lys Arg Asn Leu Arg Glu Val Asp
 370 375 380
 Tyr Thr Arg Leu Asn Lys Ala Glu Ala Glu Arg Lys Val Ala Tyr Ser
 385 390 395 400
 Asn Ile Glu Lys Leu Met Pro Phe Tyr Asn Lys Asp Leu Val Val His
 405 410 415
 Tyr Gly Asn Lys Val Ala Thr Thr Asp Lys Leu Tyr Thr Thr Glu Leu
 420 425 430
 Leu Asp Val Val Pro Met Lys Asp Asp Glu Val Val Thr Asp Ile Asn
 435 440 445
 Asn Lys Lys Asn Ser Ile Asn Lys Val Met Leu His Phe Lys Asp Asn
 450 455 460
 Thr Val Glu Tyr Leu Asp Val Thr Phe Lys Glu Asn Phe Ile Asn Ser
 465 470 475 480
 Gln Val Ile Glu Tyr Asn Val Thr Gly Lys Glu Tyr Ile Phe Thr Pro
 485 490 495
 Glu Ala Phe Val Ser Asp Tyr Thr Ala Ile Thr Asn Asn Val Leu Ser
 500 505 510
 Asp Leu Gln Asn Val Thr Leu Asn
 515 520

(2) INFORMATION FOR SEQ ID NO: 123:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 850 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 123:

CTTTGTTTTT GAAGGAAGTA AGCGTGGACA ATTTGCTGTA GAAGGAATCA ATCAACTTCG 60
 TGAGCATGTA GACACTCTAT TGATTATCTC AAACAACAAT TTGCTTGAAA TTGTTGATAA 120
 GAAAACACCG CTTTGGAGG CTCTTAGCGA AGCGGATAAC GTTCTTCGTC AAGGTGTTCA 180
 AGGGATTACC GATTTGATTA CCAATCCAGG ATTGATTAAC CTTGACTTTG CCGATGTGAA 240
 AACGGTAATG GCAAACAAAG GGAATGCTCT TATGGGTATT GGTATCGGTA GTGGAGAAGA 300
 ACGTGTGGTA GAAGCGGCAC GTAAGGCAAT CTATTCACCA CTTCTTGAAA CAACTATTGA 360

CGGTGCTGAG GATGTTATCG TCAACGTTAC TGGTGGTCTT GACTTAACCT TGATTGAGGC 420
 AGAAGAGGCT TCACAAATTG TGAACCAGGC AGCAGGTCAA GGAGTGAACA TCTGGCTCGG 480
 TACTTCAATT GATGAAAGTA TGC GTGATGA AATTCGTGTA ACAGTTGTTG CAACGGGTGT 540
 TCGTCAAGAC CGCGTAGAAA AGGTTGTGGC TCCACAAGCT AGATCTGCTA CTA ACTACCG 600
 TGAGACAGTG AAACCAGCTC ATTCACATGG CTTTGATCGT CATTTTGATA TGGCAGAAAC 660
 AGTTGAATTG CCAAAACAAA ATCCACGTCG TTTGGAACCA ACTCAGGCAT CTGCTTTTGG 720
 TGATTGGGAT CTTGCGCGTG AATCGATTGT TCGTACAACA GATTCAGTCG TTTCTCCAGT 780
 CGAGCGCTTT GAAGCCCCAA TTTCACAAGA TGAAGATGAA TTGGATACAC CTCCATTTTT 840
 CAAAAATCGT 850

(2) INFORMATION FOR SEQ ID NO:124:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 283 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:124:

Phe Gly Phe Glu Gly Ser Lys Arg Gly Gln Phe Ala Val Glu Gly Ile
 1 5 10 15
 Asn Gln Leu Arg Glu His Val Asp Thr Leu Leu Ile Ile Ser Asn Asn
 20 25 30
 Asn Leu Leu Glu Ile Val Asp Lys Lys Thr Pro Leu Leu Glu Ala Leu
 35 40 45
 Ser Glu Ala Asp Asn Val Leu Arg Gln Gly Val Gln Gly Ile Thr Asp
 50 55 60
 Leu Ile Thr Asn Pro Gly Leu Ile Asn Leu Asp Phe Ala Asp Val Lys
 65 70 75 80
 Thr Val Met Ala Asn Lys Gly Asn Ala Leu Met Gly Ile Gly Ile Gly
 85 90 95
 Ser Gly Glu Glu Arg Val Val Glu Ala Ala Arg Lys Ala Ile Tyr Ser
 100 105 110
 Pro Leu Leu Glu Thr Thr Ile Asp Gly Ala Glu Asp Val Ile Val Asn
 115 120 125
 Val Thr Gly Gly Leu Asp Leu Thr Leu Ile Glu Ala Glu Glu Ala Ser
 130 135 140
 Gln Ile Val Asn Gln Ala Ala Gly Gln Gly Val Asn Ile Trp Leu Gly
 145 150 155 160
 Thr Ser Ile Asp Glu Ser Met Arg Asp Glu Ile Arg Val Thr Val Val
 165 170 175

Ala Thr Gly Val Arg Gln Asp Arg Val Glu Lys Val Val Ala Pro Gln
180 185 190

Ala Arg Ser Ala Thr Asn Tyr Arg Glu Thr Val Lys Pro Ala His Ser
195 200 205

His Gly Phe Asp Arg His Phe Asp Met Ala Glu Thr Val Glu Leu Pro
210 215 220

Lys Gln Asn Pro Arg Arg Leu Glu Pro Thr Gln Ala Ser Ala Phe Gly
225 230 235 240

Asp Trp Asp Leu Arg Arg Glu Ser Ile Val Arg Thr Thr Asp Ser Val
245 250 255

Val Ser Pro Val Glu Arg Phe Glu Ala Pro Ile Ser Gln Asp Glu Asp
260 265 270

Glu Leu Asp Thr Pro Pro Phe Phe Lys Asn Arg
275 280

(2) INFORMATION FOR SEQ ID NO: 125:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1051 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 125:

CTACTACCTC TCGAGAGAAA GTGACCTAGA GGTGACCGTT TTTGACCATG AGCAAGGTCA	60
AGCCACCAAG GCCGCAGCAG GAATTATCAG TCCTTGGTTT TCCAAACGCC GTAATAAAGC	120
CTGGTACAAG ATGGCGCGCT TGGGGGCTGA TTTTATGTG GATTATTAG CTGATTTAGA	180
GAAATCAGGA CAAGAAATCG ACTTTTACCA GCGTTCGGGA GTCTTCTCT TGAAAAAGGA	240
TGAATCCAAT TTGGAAGAAC TTTATCAACT GGCCCTCCAG CGCAGAGAAG AATCTCCCTT	300
GATAGGGCAA TTAGCCATTC TGAACCAAGC CTCAGCTAAT GAATTATTCC CTGGTTTGCA	360
GGGATTTGAC CGCCTGCTCT ATGCTTCTGG TGGAGCGAGA GTAGATGGCC AACTTTTAGT	420
GACTCGTTTG CTGGAAGTCA GTCATGTCAA GCTGGTCAAA GAAAAAGTGA CTCTGACACC	480
GTTAGCATCA GGCTACCAGA TTGGTGAAGA GGAGTTTGAG CAGGTTATTT TGGCGACGGG	540
AGCTTGGTTG GGGGACATGT TAGAGCCTTT AGGTTATGAA GTGGATGTCC GTCCTCAAAA	600
AGGACAATA CGAGATTATC AGCTTGCCCA AGACATGGAA GATTACCCTG TTGTCATGCC	660
AGAAGGGGAG TGGGATTGA TTCCCTTGC AGGTGGGAAA TTATCCTTAG GCGCTACCCA	720
CGAAATGAC ATGGGATTTG ATTTGACGGT AGATGAAACC TTGCTCCAAC AAATGGAGGA	780
GGCCACCTTG ACTCACTATC TGATTTTGGC TGAAGCTACT TCAAATCTG AGCGTGTGG	840
AATCCGTGCC TACACCAGTG ATTTCTCTCC TTTCTTGGG CAGGTGCCTG ACTTAACTGG	900

TGTCTATGCA GCCAGTGGAC TAGGTTTCATC AGGCCTCACA ACTGGTCCTA TCATTGGTTA 960
 CCATCTAGCC CAACTGATCC AAGACAAGGA GTTGACCTTG GACCCTCTAA ATTACCCAAT 1020
 TGAAAACTAT GTCAAACGAG TAAAAAGCGA A 1051

(2) INFORMATION FOR SEQ ID NO:126:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 350 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:126:

Tyr Tyr Leu Ser Arg Glu Ser Asp Leu Glu Val Thr Val Phe Asp His
 1 5 10 15
 Glu Gln Gly Gln Ala Thr Lys Ala Ala Ala Gly Ile Ile Ser Pro Trp
 20 25 30
 Phe Ser Lys Arg Arg Asn Lys Ala Trp Tyr Lys Met Ala Arg Leu Gly
 35 40 45
 Ala Asp Phe Tyr Val Asp Leu Leu Ala Asp Leu Glu Lys Ser Gly Gln
 50 55 60
 Glu Ile Asp Phe Tyr Gln Arg Ser Gly Val Phe Leu Leu Lys Lys Asp
 65 70 75 80
 Glu Ser Asn Leu Glu Glu Leu Tyr Gln Leu Ala Leu Gln Arg Arg Glu
 85 90 95
 Glu Ser Pro Leu Ile Gly Gln Leu Ala Ile Leu Asn Gln Ala Ser Ala
 100 105 110
 Asn Glu Leu Phe Pro Gly Leu Gln Gly Phe Asp Arg Leu Leu Tyr Ala
 115 120 125
 Ser Gly Gly Ala Arg Val Asp Gly Gln Leu Leu Val Thr Arg Leu Leu
 130 135 140
 Glu Val Ser His Val Lys Leu Val Lys Glu Lys Val Thr Leu Thr Pro
 145 150 155 160
 Leu Ala Ser Gly Tyr Gln Ile Gly Glu Glu Glu Phe Glu Gln Val Ile
 165 170 175
 Leu Ala Thr Gly Ala Trp Leu Gly Asp Met Leu Glu Pro Leu Gly Tyr
 180 185 190
 Glu Val Asp Val Arg Pro Gln Lys Gly Gln Leu Arg Asp Tyr Gln Leu
 195 200 205
 Ala Gln Asp Met Glu Asp Tyr Pro Val Val Met Pro Glu Gly Glu Trp
 210 215 220
 Asp Leu Ile Pro Phe Ala Gly Gly Lys Leu Ser Leu Gly Ala Thr His

09763274 043200

(2) INFORMATION FOR SEO ID NO: 127:

(A) LENGTH: 352 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

TAAGGTCAAA	AGTCAGACCG	CTAAGAAAGT	GCTAGAAAAG	ATTGGAGCTG	ACTCGGTTAT	60
CTCGCCAGAG	TATGAAATGG	GGCAGTCTCT	AGCACAGACC	ATTCTTTTCC	ATAATAGTGT	120
TGATGTC'TTT	CAGTTGGATA	AAAATGTGTC	TATCGTGGAG	ATGAAAATTC	CTCAGTCTTG	180
GGCAGGTCAA	AGTCTGAGTA	AATTAGACCT	CCGTGGCAAA	TACAATCTGA	ATATTTTGGG	240
TTTCCGAGAG	CAGGAAAATT	CCCCATTGGA	TGTTGAATTT	GGACCAGATG	ACCTCTTGAA	300
AGCAGATACC	TATATTTTGG	CAGTCATCAA	CAACCAGTAT	TTGGATACCC	TA	352

(A) LENGTH: 117 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:128:

Lys Val Lys Ser Gln Thr Ala Lys Lys Val Leu Glu Lys Ile Gly Ala
1 5 10 15

(2) INFORMATION FOR SEQ ID NO: 129:

(A) LENGTH: 247 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

TGACGGGTCT	CAGGATCAGA	CTCAGGAAAT	CGCTGAGTGT	TTAGCTAGCA	AGTATCCTAA	60
TATCGTTAGA	GCCATCTATC	AGGAAAATAA	ATGCCATGGC	GGTGCGGTCA	ATCGTGGCTT	120
GGTAGAGGCT	TCTGGGCGCT	ATTTTAAAGT	AGTTGACAGT	GATGACTGGG	TGGATCCTCG	180
TGCCTACTTG	AAAATTCTTG	AAACTTGCAG	GAACTTGAGA	GCAAAGGTCA	AGAGGTGGAT	240
GTCTTTG						247

(A) LENGTH: 82 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:130:

Asp Gly Ser Gln Asp Gln Thr Gln Glu Ile Ala Glu Cys Leu Ala Ser
 1 5 10 15
 Lys Tyr Pro Asn Ile Val Arg Ala Ile Tyr Gln Glu Asn Lys Cys His
 20 25 30
 Gly Gly Ala Val Asn Arg Gly Leu Val Glu Ala Ser Gly Arg Tyr Phe

45

Ser Leu

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1744 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

TAGAGGCTTT	GCCAAATGGT	GGGAAGGGCA	CGAGCGTCGA	AAAGAGGAAC	GCTTTGTCAA	60
ACAAGAAGAA	AAAGCTCGCC	AAAAGGCTGA	GAAAGAGGCT	AGATTAGAAC	AAGAAGAGAC	120
TGAAAAAGCC	TTACTCGATT	TGCCTCCTGT	TGATATGGAA	ACGGGTGAAA	TTCTGACAGA	180
GGAAGCTGTT	CAAAATCTTC	CACCTATTCC	AGAAGAAAAG	TGGGTGGAAC	CAGAAAATCAT	240
CCTGCCTCAA	GCTGAACTTA	AATTCCCTGA	ACAGGAAGAT	GACTCAGATG	ACGAAGATGT	300
TCAGGTCGAT	TTTTCAGCCA	AAGAAGCCCT	TGAATACAAA	CTTCCAAGCT	TACAACTCTT	360
TGCACCAGAT	AAACCAAAG	ATCAGTCTAA	AGAGAAGAAA	ATTGTCAGAG	AAAATATCAA	420
AATCTTAGAA	GCAACCTTTG	CTAGCTTTGG	TATTAAGGTA	ACAGTTGAAC	GGGCCGAAAT	480
TGGGCCATCA	GTGACCAAGT	ATGAAGTCAA	GCCGGCTGTT	GGTGTAAGGG	TCAACCGCAT	540
TTCCAATCTA	TCAGATGACC	TCGCTCTAGC	CTTGGCTGCC	AAAGATGTCC	GGATTGAAGC	600
ACCAATCCCT	GGGAAATCCC	TAATCGGAAT	TGAAGTGCCC	AACTCCGATA	TTGCCACTGT	660
ATCTTTCCGA	GAACATATGGG	AACAATCGCA	AACGAAAGCA	GAAAATTTCT	TGGAAAATTCC	720
TTTAGGGAAG	GCTGTTAATG	GAACCGCAAG	AGCTTTTGAC	CTTTCTAAAA	TGCCCCACTT	780
GCTAGTTGCA	GGTTCAACGG	GTTCAGGGAA	GTCAGTAGCA	GTTAACGGCA	TTATTGCTAG	840
CATTCTCATG	AAGGCGAGAC	CAGATCAAGT	TAAATTTATG	ATGGTCGATC	CCAAGATGGT	900
TGAGTTATCT	GTTTACAATG	ATATTCCCCA	CCTCTTGATT	CCAGTCGTGA	CCAATCCACG	960
CAAAGCCAGC	AAGGCTCTGC	AAAAGGTTGT	GGATGAAATG	GAAAACCGTT	ATGAACTCTT	1020
TGCCAAGGTG	GGAGTTCGGA	ATATTGCAGG	TTTTAATGCC	AAGGTAGAAG	AGTTCAATTC	1080
CCAGTCTGAG	TACAAGCAAA	TTCCGCTACC	ATTCATTGTC	GTGATTGTGG	ATGAGTTGGC	1140
TGACCTCATG	ATGGTGGCCA	GCAAGGAAGT	GGAAGATGCT	ATCATCCGTC	TTGGGCAGAA	1200

GGCGCGTGCT GCAGGTATCC ACATGATTCT TGCAACTCAG CGTCCATCTG TTGATGTCAT 1260
 CTCTGGTTTG ATTAAGGCCA ATGTTCCATC TCGTGTAGCA TTTGCGGTTT CATCAGGAAC 1320
 AGACTCCCGT ACGATTTTGG ATGAAAATGG AGCAGAAAAA CTTCTTGGTC GAGGAGACAT 1380
 GCTCTTTAAA CCGATTGATG AAAATCATCC AGTTCGTCTC CAAGGCTCCT TTATCTCGGA 1440
 TGACGATGTT GAGCGCATTG TGAAC TTCAT CAAGACTCAG GCAGATGCAG ACTACGATGA 1500
 GAGTTTTGAT CCAGGTGAGG TTTCTGAAAA TGAAGGAGAA TTTTCGGATG GAGATGCTGG 1560
 TGGTGATCCG CTTTTTGAAG AAGCTAAGTC TTTGGTTATC GAAACACAGA AAGCCAGTGC 1620
 GTCTATGATT CAGCGTCGTT TATCAGTTGG ATTTAACCGT GCGACCCGTC TCATGGAAGA 1680
 ACTGGAGATA GCAGGTGTCA TCGGTCCAGC TGAAGGTACC AAACCTCGAA AAGTGTTACA 1740
 ACAA 1744

(2) INFORMATION FOR SEQ ID NO:132:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 581 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:132:

Arg Gly Phe Ala Lys Trp Trp Glu Gly His Glu Arg Arg Lys Glu Glu
 1 5 10 15
 Arg Phe Val Lys Gln Glu Glu Lys Ala Arg Gln Lys Ala Glu Lys Glu
 20 25 30
 Ala Arg Leu Glu Gln Glu Glu Thr Glu Lys Ala Leu Leu Asp Leu Pro
 35 40 45
 Pro Val Asp Met Glu Thr Gly Glu Ile Leu Thr Glu Glu Ala Val Gln
 50 55 60
 Asn Leu Pro Pro Ile Pro Glu Glu Lys Trp Val Glu Pro Glu Ile Ile
 65 70 75 80
 Leu Pro Gln Ala Glu Leu Lys Phe Pro Glu Gln Glu Asp Asp Ser Asp
 85 90 95
 Asp Glu Asp Val Gln Val Asp Phe Ser Ala Lys Glu Ala Leu Glu Tyr
 100 105 110
 Lys Leu Pro Ser Leu Gln Leu Phe Ala Pro Asp Lys Pro Lys Asp Gln
 115 120 125
 Ser Lys Glu Lys Lys Ile Val Arg Glu Asn Ile Lys Ile Leu Glu Ala
 130 135 140
 Thr Phe Ala Ser Phe Gly Ile Lys Val Thr Val Glu Arg Ala Glu Ile
 145 150 155 160

Gly	Pro	Ser	Val	Thr	Lys	Tyr	Glu	Val	Lys	Pro	Ala	Val	Gly	Val	Arg
			165						170					175	
Val	Asn	Arg	Ile	Ser	Asn	Leu	Ser	Asp	Asp	Leu	Ala	Leu	Ala	Leu	Ala
			180					185					190		
Ala	Lys	Asp	Val	Arg	Ile	Glu	Ala	Pro	Ile	Pro	Gly	Lys	Ser	Leu	Ile
		195					200					205			
Gly	Ile	Glu	Val	Pro	Asn	Ser	Asp	Ile	Ala	Thr	Val	Ser	Phe	Arg	Glu
	210					215					220				
Leu	Trp	Glu	Gln	Ser	Gln	Thr	Lys	Ala	Glu	Asn	Phe	Leu	Glu	Ile	Pro
225					230					235					240
Leu	Gly	Lys	Ala	Val	Asn	Gly	Thr	Ala	Arg	Ala	Phe	Asp	Leu	Ser	Lys
				245					250					255	
Met	Pro	His	Leu	Leu	Val	Ala	Gly	Ser	Thr	Gly	Ser	Gly	Lys	Ser	Val
			260					265					270		
Ala	Val	Asn	Gly	Ile	Ile	Ala	Ser	Ile	Leu	Met	Lys	Ala	Arg	Pro	Asp
		275					280					285			
Gln	Val	Lys	Phe	Met	Met	Val	Asp	Pro	Lys	Met	Val	Glu	Leu	Ser	Val
	290					295					300				
Tyr	Asn	Asp	Ile	Pro	His	Leu	Leu	Ile	Pro	Val	Val	Thr	Asn	Pro	Arg
305					310					315					320
Lys	Ala	Ser	Lys	Ala	Leu	Gln	Lys	Val	Val	Asp	Glu	Met	Glu	Asn	Arg
				325					330					335	
Tyr	Glu	Leu	Phe	Ala	Lys	Val	Gly	Val	Arg	Asn	Ile	Ala	Gly	Phe	Asn
			340					345					350		
Ala	Lys	Val	Glu	Glu	Phe	Asn	Ser	Gln	Ser	Glu	Tyr	Lys	Gln	Ile	Pro
		355					360					365			
Leu	Pro	Phe	Ile	Val	Val	Ile	Val	Asp	Glu	Leu	Ala	Asp	Leu	Met	Met
	370					375					380				
Val	Ala	Ser	Lys	Glu	Val	Glu	Asp	Ala	Ile	Ile	Arg	Leu	Gly	Gln	Lys
385					390					395					400
Ala	Arg	Ala	Ala	Gly	Ile	His	Met	Ile	Leu	Ala	Thr	Gln	Arg	Pro	Ser
				405					410					415	
Val	Asp	Val	Ile	Ser	Gly	Leu	Ile	Lys	Ala	Asn	Val	Pro	Ser	Arg	Val
			420					425					430		
Ala	Phe	Ala	Val	Ser	Ser	Gly	Thr	Asp	Ser	Arg	Thr	Ile	Leu	Asp	Glu
		435					440					445			
Asn	Gly	Ala	Glu	Lys	Leu	Leu	Gly	Arg	Gly	Asp	Met	Leu	Phe	Lys	Pro
	450					455					460				
Ile	Asp	Glu	Asn	His	Pro	Val	Arg	Leu	Gln	Gly	Ser	Phe	Ile	Ser	Asp
465					470					475					480
Asp	Asp	Val	Glu	Arg	Ile	Val	Asn	Phe	Ile	Lys	Thr	Gln	Ala	Asp	Ala
				485					490					495	

Asp Tyr Asp Glu Ser Phe Asp Pro Gly Glu Val Ser Glu Asn Glu Gly
500 505 510

Glu Phe Ser Asp Gly Asp Ala Gly Gly Asp Pro Leu Phe Glu Glu Ala
515 520 525

Lys Ser Leu Val Ile Glu Thr Gln Lys Ala Ser Ala Ser Met Ile Gln
530 535 540

Arg Arg Leu Ser Val Gly Phe Asn Arg Ala Thr Arg Leu Met Glu Glu
545 550 555 560

Leu Glu Ile Ala Gly Val Ile Gly Pro Ala Glu Gly Thr Lys Pro Arg
565 570 575

Lys Val Leu Gln Gln
580

(2) INFORMATION FOR SEQ ID NO: 133:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 829 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 133:

TCAAAAAGAG AAGGAAACT TGTTATTGC TGGGAAAATA GGTCCAGAAC CAGAAATTTT	60
GGCCAATATG TATAAGTTGC TGATTGAAGA AAATACCAGC ATGACTGCGA CTGTTAAACC	120
GAATTTTGGG AAGACAAGCT TCCTTTATGA AGCTCTGAAA AAAGGCGATA TTGACATCTA	180
TCCTGAATTT ACTGGTACGG TGAAGTAAAG TTTGCTTCAA CCATCACCCA AGGTGAGTCA	240
TGAACCAGAA CAGGTTTATC AGGTGGCGCG TGATGGCATT GCTAAGCAGG ATCATCTAGC	300
CTATCTCAAA CCCATGTCTT ATCAAAACAC CTATGCTGTA GCTGTTCCGA AAAAGATTGC	360
TCAAGAATAT GGCTTGAAGA CCATTTTCTA CTTGAAAAAA GTGGAAGGGC AGTTGAAGGC	420
AGGTTTTTACA CTCGAGTTTA ACGACCGTGA AGATGGAAAT AAGGGCTTGC AATCAATGTA	480
TGGTCTCAAT CTCAATGTAG CGACCATTGA GCCAGCCCTT CGCTATCAGG CTATTCAGTC	540
AGGGGATATT CAAATCACGG ATGCCTATTC GACTGATGCG GAATTGGAGC GTTATGATTT	600
ACAGGTCTTG GAAGATGACA AGCAACTCTT CCCACCTTAT CAAGGGGCTC CACTCATGAA	660
AGAAGCTCTT CTCAAGAAAC ACCCAGAGTT GGAAAGAGTT CTTAATACAT TGGCTGGTAA	720
GATTACAGAA AGCCAGATGA GCCAGCTCAA CTACCAAGTC GGTGTTGAAG GCAAGTCAGC	780
AAAGCAAGTA GCCAAGGAGT TTCTCCAAGA ACAAGGTTTG TTGAAGAAA	829

(2) INFORMATION FOR SEQ ID NO:134:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 276 amino acids
- (B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:134:

Gln Lys Glu Lys Glu Asn Leu Val Ile Ala Gly Lys Ile Gly Pro Glu
 1 5 10 15
 Pro Glu Ile Leu Ala Asn Met Tyr Lys Leu Leu Ile Glu Glu Asn Thr
 20 25 30
 Ser Met Thr Ala Thr Val Lys Pro Asn Phe Gly Lys Thr Ser Phe Leu
 35 40 45
 Tyr Glu Ala Leu Lys Lys Gly Asp Ile Asp Ile Tyr Pro Glu Phe Thr
 50 55 60
 Gly Thr Val Thr Glu Ser Leu Leu Gln Pro Ser Pro Lys Val Ser His
 65 70 75 80
 Glu Pro Glu Gln Val Tyr Gln Val Ala Arg Asp Gly Ile Ala Lys Gln
 85 90 95
 Asp His Leu Ala Tyr Leu Lys Pro Met Ser Tyr Gln Asn Thr Tyr Ala
 100 105 110
 Val Ala Val Pro Lys Lys Ile Ala Gln Glu Tyr Gly Leu Lys Thr Ile
 115 120 125
 Ser Asp Leu Lys Lys Val Glu Gly Gln Leu Lys Ala Gly Phe Thr Leu
 130 135 140
 Glu Phe Asn Asp Arg Glu Asp Gly Asn Lys Gly Leu Gln Ser Met Tyr
 145 150 155 160
 Gly Leu Asn Leu Asn Val Ala Thr Ile Glu Pro Ala Leu Arg Tyr Gln
 165 170 175
 Ala Ile Gln Ser Gly Asp Ile Gln Ile Thr Asp Ala Tyr Ser Thr Asp
 180 185 190
 Ala Glu Leu Glu Arg Tyr Asp Leu Gln Val Leu Glu Asp Asp Lys Gln
 195 200 205
 Leu Phe Pro Pro Tyr Gln Gly Ala Pro Leu Met Lys Glu Ala Leu Leu
 210 215 220
 Lys Lys His Pro Glu Leu Glu Arg Val Leu Asn Thr Leu Ala Gly Lys
 225 230 235 240
 Ile Thr Glu Ser Gln Met Ser Gln Leu Asn Tyr Gln Val Gly Val Glu
 245 250 255
 Gly Lys Ser Ala Lys Gln Val Ala Lys Glu Phe Leu Gln Glu Gln Gly
 260 265 270
 Leu Leu Lys Lys
 275

(2) INFORMATION FOR SEQ ID NO: 135:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 712 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 135:

ACGTTCTATT GAGGACCACT TTGATTCAAA CTTCGAATTG GAATATAACC TCAAAGAAAA 60
 AGGGAAAACA GATCTTTTGA AGCTAGTTGA TAAACAACCT GACATGCGTC TGCATTTTAT 120
 CCGCCAAACT CATCCACGCG GTCTCGGAGA TGCTGTTTTG CAAGCCAAGG CTTTCGTCGG 180
 AAATGAACCT TTTGTCGTTA TGCTTGGTGA TGACTTGATG GATATCACAG ACGAAAAGGC 240
 TGTTCCTACTT ACCAAACAAC TCATGGATGA CTACGAGCGT ACCCAGCGCT CTAATATCGC 300
 TGTCATGCCA GTCCCTCATG ACGAAGTATC TGCTTACGGG GTTATTGCTC CGCAAGGCGA 360
 AGGAAAAGAT GGTCTTTACA GTGTTGAAAC CTTTGTGTGA AAACCAGCTC CAGAGGACGC 420
 TCCTAGCGAC CTTGCTATTA TCGGACGCTA CCTCCTCACG CCTGAAATTT TTGAGATTCT 480
 CGAAAAGCAA GCTCCAGGTG CAGGAAATGA AATTCAGCTG ACAGATGCAA TCGACACCCCT 540
 CAATAAAACA CAACGTGTAT TTGCTCGTGA GTTCAAAGGG GCTCGTTACG ATGTCGGAGA 600
 CAAGTTTGGC TTCATGAAAA CATCCATCGA CTACGCCCTC AAACACCCAC AAGTCAAAGA 660
 TGATTTGAAG AATTACCTCA TCCAACCTGG AAAAGAATTG ACTGAGAAGG AA 712

(2) INFORMATION FOR SEQ ID NO:136:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 237 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:136:

Arg Ser Ile Glu Asp His Phe Asp Ser Asn Phe Glu Leu Glu Tyr Asn
 1 5 10 15
 Leu Lys Glu Lys Gly Lys Thr Asp Leu Leu Lys Leu Val Asp Lys Thr
 20 25 30
 Thr Asp Met Arg Leu His Phe Ile Arg Gln Thr His Pro Arg Gly Leu
 35 40 45
 Gly Asp Ala Val Leu Gln Ala Lys Ala Phe Val Gly Asn Glu Pro Phe
 50 55 60
 Val Val Met Leu Gly Asp Asp Leu Met Asp Ile Thr Asp Glu Lys Ala
 65 70 75 80

251

Val	Pro	Leu	Thr	Lys	Gln	Leu	Met	Asp	Asp	Tyr	Glu	Arg	Thr	His	Ala	
				85					90					95		
Ser	Thr	Ile	Ala	Val	Met	Pro	Val	Pro	His	Asp	Glu	Val	Ser	Ala	Tyr	
			100					105					110			
Gly	Val	Ile	Ala	Pro	Gln	Gly	Glu	Gly	Lys	Asp	Gly	Leu	Tyr	Ser	Val	
		115					120					125				
Glu	Thr	Phe	Val	Glu	Lys	Pro	Ala	Pro	Glu	Asp	Ala	Pro	Ser	Asp	Leu	
	130					135					140					
Ala	Ile	Ile	Gly	Arg	Tyr	Leu	Leu	Thr	Pro	Glu	Ile	Phe	Glu	Ile	Leu	
145					150					155					160	
Glu	Lys	Gln	Ala	Pro	Gly	Ala	Gly	Asn	Glu	Ile	Gln	Leu	Thr	Asp	Ala	
			165					170						175		
Ile	Asp	Thr	Leu	Asn	Lys	Thr	Gln	Arg	Val	Phe	Ala	Arg	Glu	Phe	Lys	
			180					185					190			
Gly	Ala	Arg	Tyr	Asp	Val	Gly	Asp	Lys	Phe	Gly	Phe	Met	Lys	Thr	Ser	
		195					200					205				
Ile	Asp	Tyr	Ala	Leu	Lys	His	Pro	Gln	Val	Lys	Asp	Asp	Leu	Lys	Asn	
	210					215					220					
Tyr	Leu	Ile	Gln	Leu	Gly	Lys	Glu	Leu	Thr	Glu	Lys	Glu				
225					230					235						

(2) INFORMATION FOR SEQ ID NO: 137:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 502 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 137:

CGCTCAAAAT ACCAGAGGTG TTCAGCTAAT CGAGCACGTT TCTCCTCAAA TGTTGAAAGC	60
CCAATTGGAG AGTGTCTTTT CTGATATTCC ACCTCAGGCT GTAAAACTG GAATGTTGGC	120
TACTACTGAA ATCATGGAAA TCATCCAACC CTATCTTAAA AAAGTGGATT GTCCCTATGT	180
CCTTGATCCT GTTATGGTTG CTACAAGTGG AGATGCCTTG ATTGACTCAA ATGCTAGAGA	240
CTATCTCAAA ACAAACTTAC TACCTCTAGC AACTATTATT ACGCCAAATC TTCCTGAAGC	300
AGAAGAGATT GTTGGTTTTT CAATCCATGA CCCCAGAGAC ATGCAGCGTG CTGGTCGCCT	360
GATTTTAAAA GAATTGGTC CTCAGTCTGT GGTTATCAAA GCGGACATC TCAAAGGTGG	420
TGCTAAAGAT TTCCTCTTTA CCAAGAATGA ACAATTTGTC TGGGAAAGCC CACGAATTCA	480
AACCTGTCAC ACCCATGGTA CT	502

(2) INFORMATION FOR SEQ ID NO:138:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 167 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:138:

Ala	Gln	Asn	Thr	Arg	Gly	Val	Gln	Leu	Ile	Glu	His	Val	Ser	Pro	Gln	1	5	10	15
Met	Leu	Lys	Ala	Gln	Leu	Glu	Ser	Val	Phe	Ser	Asp	Ile	Pro	Pro	Gln	20	25	30	
Ala	Val	Lys	Thr	Gly	Met	Leu	Ala	Thr	Thr	Glu	Ile	Met	Glu	Ile	Ile	35	40	45	
Gln	Pro	Tyr	Leu	Lys	Lys	Leu	Asp	Cys	Pro	Tyr	Val	Leu	Asp	Pro	Val	50	55	60	
Met	Val	Ala	Thr	Ser	Gly	Asp	Ala	Leu	Ile	Asp	Ser	Asn	Ala	Arg	Asp	65	70	75	80
Tyr	Leu	Lys	Thr	Asn	Leu	Leu	Pro	Leu	Ala	Thr	Ile	Ile	Thr	Pro	Asn	85	90	95	
Leu	Pro	Glu	Ala	Glu	Glu	Ile	Val	Gly	Phe	Ser	Ile	His	Asp	Pro	Glu	100	105	110	
Asp	Met	Gln	Arg	Ala	Gly	Arg	Leu	Ile	Leu	Lys	Glu	Phe	Gly	Pro	Gln	115	120	125	
Ser	Val	Val	Ile	Lys	Gly	Gly	His	Leu	Lys	Gly	Gly	Ala	Lys	Asp	Phe	130	135	140	
Leu	Phe	Thr	Lys	Asn	Glu	Gln	Phe	Val	Trp	Glu	Ser	Pro	Arg	Ile	Gln	145	150	155	160
Thr	Cys	His	Thr	His	Gly	Thr										165			

(2) INFORMATION FOR SEQ ID NO: 139:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 805 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 139:

AATTGTACAA	TTAGAAAAG	ATAGCAAATC	AGACAAAGAA	CAAGTTGATA	AACTATTTGA	60
ATCATTTGAT	GCATCTTCAG	ATGAATCTAT	TTCTAAATTA	AAAGAACTAT	CTGAAACTTC	120
ACTTAAACC	GATGCAGGTA	AAGACTATCT	TAATAACAAA	GTCAAAGAAT	CATCTAAAGC	180
AATTGTAGAT	TTTCATTGTC	AAAAGGTTT	GGCTTATGAT	GTAAAGATT	CAGATGACAA	240

ATTTAAAGAT AAAGCAACTC TTGAAACAAA TGTAAGAGAA ATTACAAAAC AAATTGATTT 300
 TATCAAAAAA GTTGATGAAA CTTTTAAACA AGAGAATTG GAAGAACTC TTAAATCTCT 360
 AAATGATCTT GTTGATAAAT ATCAAAAACA AATCGAAGTT TTGAAGAAAG AAGAAGAAAA 420
 AGCTGCTGAA AAAGCTGCTG AAAAAGCAAA GGAATCTTCT AGTCAAAGTA ATTCTTCTGG 480
 TAGTGCTTCT AATGAGTCTT ATAATGGATC TTCCAATTCA AATGTAGATT ATAGTTCATC 540
 TGAACAAACT AATGGATATT CAAATAATTA TGGCGGTCAA GATTATTCTG GTTCAGGAGA 600
 TAGTTCAACA AATGGTGGAT CATCAGAACA ATATTCATCT AGCAATTCAA ACAGCGGAGC 660
 AAATAATGTC TACAGATATA AAGGCACTGG TGCTGACGGC TATCAAAGAT ACTACTACAA 720
 AGATCATAAT AATGGAGATG TGTATGATGA CGATGGAAAT TACCTTGGA ACTTTGGTGG 780
 CGGCATTGCA GAACCTAGTC AACGC 805

(2) INFORMATION FOR SEQ ID NO:140:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 268 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:140:

Ile Val Gln Leu Glu Lys Asp Ser Lys Ser Asp Lys Glu Gln Val Asp
 1 5 10 15
 Lys Leu Phe Glu Ser Phe Asp Ala Ser Ser Asp Glu Ser Ile Ser Lys
 20 25 30
 Leu Lys Glu Leu Ser Glu Thr Ser Leu Lys Thr Asp Ala Gly Lys Asp
 35 40 45
 Tyr Leu Asn Asn Lys Val Lys Glu Ser Ser Lys Ala Ile Val Asp Phe
 50 55 60
 His Leu Gln Lys Gly Leu Ala Tyr Asp Val Lys Asp Ser Asp Asp Lys
 65 70 75 80
 Phe Lys Asp Lys Ala Thr Leu Glu Thr Asn Val Lys Glu Ile Thr Lys
 85 90 95
 Gln Ile Asp Phe Ile Lys Lys Val Asp Glu Thr Phe Lys Gln Glu Asn
 100 105 110
 Leu Glu Glu Thr Leu Lys Ser Leu Asn Asp Leu Val Asp Lys Tyr Gln
 115 120 125
 Lys Gln Ile Glu Leu Leu Lys Lys Glu Glu Glu Lys Ala Ala Glu Lys
 130 135 140
 Ala Ala Glu Lys Ala Lys Glu Ser Ser Ser Gln Ser Asn Ser Ser Gly
 145 150 155 160

Ser Ala Ser Asn Glu Ser Tyr Asn Gly Ser Ser Asn Ser Asn Val Asp
 165 170 175

Tyr Ser Ser Ser Glu Gln Thr Asn Gly Tyr Ser Asn Asn Tyr Gly Gly
 180 185 190

Gln Asp Tyr Ser Gly Ser Gly Asp Ser Ser Thr Asn Gly Gly Ser Ser
 195 200 205

Glu Gln Tyr Ser Ser Ser Asn Ser Asn Ser Gly Ala Asn Asn Val Tyr
 210 215 220

Arg Tyr Lys Gly Thr Gly Ala Asp Gly Tyr Gln Arg Tyr Tyr Tyr Lys
 225 230 235 240

Asp His Asn Asn Gly Asp Val Tyr Asp Asp Asp Gly Asn Tyr Leu Gly
 245 250 255

Asn Phe Gly Gly Gly Ile Ala Glu Pro Ser Gln Arg
 260 265

(2) INFORMATION FOR SEQ ID NO: 141:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 211 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 141:

TCTGACCAAG CAAAAGAAG CAGTCAATGA CAAAGGAAAA GCAGCTGTTG TTAAGGTGGT 60

GGAAAGCCAG GCAGAACTTT ATAGCTTAGA AAAGAATGAA GATGCTAGCC TAAGAAAGTT 120

ACAAGCAGAT GGACGCATCA CGGAAGAACA GGCTAAAGCT TATAAAGAAT ACAATGATAA 180

AAATGGAGGA GCAAATCGTA AAGTCAATGA T 211

(2) INFORMATION FOR SEQ ID NO:142:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 70 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:142:

Leu Thr Lys Gln Lys Glu Ala Val Asn Asp Lys Gly Lys Ala Ala Val
 1 5 10 15

Val Lys Val Val Glu Ser Gln Ala Glu Leu Tyr Ser Leu Glu Lys Asn
 20 25 30

Glu Asp Ala Ser Leu Arg Lys Leu Gln Ala Asp Gly Arg Ile Thr Glu
 35 40 45

Glu Gln Ala Lys Ala Tyr Lys Glu Tyr Asn Asp Lys Asn Gly Gly Ala
 50 55 60

Asn Arg Lys Val Asn Asp
 65 70

(2) INFORMATION FOR SEQ ID NO: 143:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 331 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 143:

GTCCGGCTCT GTCCAGTCCA CTTTTTCAGC GGTAGAGGAA CAGATTTTCT TTATGGAGTT	60
TGAAGAACTC TATCGGGAAA CCCAAAAACG CAGTGTAGCC AGTCAGCAAA AGACTAGTCT	120
GAACCTAGAT GGGCAGACGC TTAGCAATGG CAGTCAAAAG TTGCCAGTCC CTAAAGGAAT	180
TCAGGCCCCA TCAGGCCAAA GTATTACATT TGACCGAGCT GGGGGCAATT CGTCCCTGGC	240
TAAGGTTGAA TTTAGACCA GTAAAGGAGC GATTGCTAT CAATTATATC TAGGAAATGG	300
AAAAATTAAA CGCATTAAAGG AAACAAAAAA T	331

(2) INFORMATION FOR SEQ ID NO:144:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 110 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:144:

Ser Gly Ser Val Gln Ser Thr Phe Ser Ala Val Glu Glu Gln Ile Phe	
1 5 10 15	
Phe Met Glu Phe Glu Glu Leu Tyr Arg Glu Thr Gln Lys Arg Ser Val	
20 25 30	
Ala Ser Gln Gln Lys Thr Ser Leu Asn Leu Asp Gly Gln Thr Leu Ser	
35 40 45	
Asn Gly Ser Gln Lys Leu Pro Val Pro Lys Gly Ile Gln Ala Pro Ser	
50 55 60	
Gly Gln Ser Ile Thr Phe Asp Arg Ala Gly Gly Asn Ser Ser Leu Ala	
65 70 75 80	
Lys Val Glu Phe Gln Thr Ser Lys Gly Ala Ile Arg Tyr Gln Leu Tyr	
85 90 95	
Leu Gly Asn Gly Lys Ile Lys Arg Ile Lys Glu Thr Lys Asn	
100 105 110	

(2) INFORMATION FOR SEQ ID NO: 145:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 196 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 145:

GGGACAAATT CAAAAAATA GGCAAGAGGA AGCAAAAATC TTGCAAAAGG AAGAAGTCTT 60
 GAGGGTAGCT AAGATGGCCC TGCAGACGGG GCAAAATCAG GTAAGCATCA ACGGAGTTGA 120
 GATTCAGGTA TTTTCTAGTG AAAAAGGATT GGAGGTCTAC CATGGTTCAG AACAGTTGTT 180
 GGCAATCAAA GAGCCA 196

(2) INFORMATION FOR SEQ ID NO:146:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 65 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:146:

Gly Gln Ile Gln Lys Asn Arg Gln Glu Glu Ala Lys Ile Leu Gln Lys
 1 5 10 15
 Glu Glu Val Leu Arg Val Ala Lys Met Ala Leu Gln Thr Gly Gln Asn
 20 25 30
 Gln Val Ser Ile Asn Gly Val Glu Ile Gln Val Phe Ser Ser Glu Lys
 35 40 45
 Gly Leu Glu Val Tyr His Gly Ser Glu Gln Leu Leu Ala Ile Lys Glu
 50 55 60
 Pro
 65

(2) INFORMATION FOR SEQ ID NO: 147:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 319 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 147:

TCGCTACCAG CAACAAAGCG AGCAAAAGGA GTGGCTCTTG TTTGTGGACC AACTTGAGGT 60

097554 042299260

AGAATTAGAC CGTTCGCAGT TCGAAAAAGT AGAAGGCAAT CGCCTATACA TGAAGCAAGA 120
 TGGCAAGGAC ATCGCCATCG GTAAGTCAAA GTCAGATGAT TTCCGTAAAA CGAATGCTCG 180
 TGGTCGAGGT TATCAGCCTA TGGTTTATGG ACTCAAATCT GTACGGATTA CAGAGGACAA 240
 TCAACTGGTT CGCTTTCATT TCCAGTTCCA AAAAGGCTTA GAAAGGGAGT TCATCTATCG 300
 TGTGGAAAAA GAAAAAAGT 319

(2) INFORMATION FOR SEQ ID NO:148:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 106 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:148:

Arg Tyr Gln Gln Gln Ser Glu Gln Lys Glu Trp Leu Leu Phe Val Asp
 1 5 10 15
 Gln Leu Glu Val Glu Leu Asp Arg Ser Gln Phe Glu Lys Val Glu Gly
 20 25 30
 Asn Arg Leu Tyr Met Lys Gln Asp Gly Lys Asp Ile Ala Ile Gly Lys
 35 40 45
 Ser Lys Ser Asp Asp Phe Arg Lys Thr Asn Ala Arg Gly Arg Gly Tyr
 50 55 60
 Gln Pro Met Val Tyr Gly Leu Lys Ser Val Arg Ile Thr Glu Asp Asn
 65 70 75 80
 Gln Leu Val Arg Phe His Phe Gln Phe Gln Lys Gly Leu Glu Arg Glu
 85 90 95
 Phe Ile Tyr Arg Val Glu Lys Glu Lys Ser
 100 105

(2) INFORMATION FOR SEQ ID NO: 149:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 322 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 149:

GAACCGACAA GTCGCCCACT ATCAAGACTA TGCTTTGAAT AAAGAAAAAT TGGTTGCTTT 60
 TGCTATGGCT AAACGAACCA AAGATAAGGT TGAGCAAGAA AGTGGGGAAC AGTTTTTTAA 120
 TCTAGGTCAG GTAAGCTATC AAAACAAGAA AACTGGCTTA GTGACGAGGG TTCGTACGGA 180
 TAAGAGCCAA TATGAGTTTC TGTTTCCTTC AGTCAAAATC AAAGAAGAGA AAAGAGATAA 240

(2) INFORMATION FOR SEQ ID NO:150:

- (ii) MOLECULE TYPE: protein

- Ser Glu Glu Lys Pro Glu Lys Lys Glu Asn Ser
100 105

- | | | | | | | |
|------------|------------|------------|------------|------------|------------|-----|
| GGTTGTCGGC | TGGCAATATA | TCCCGTTTCC | ATCTAAAGGT | AGTACAATTG | GTCTTACCC | 60 |
| AAATGGTATC | AGATTAGAAG | GTTTTCCAAA | GTCAGAGTGG | TACTACTTCG | ATAAAAATGG | 120 |
| AGTGCTACAA | GAGTTTGTTG | GTTGGAAAAC | ATTAGAGATT | AAAACTAAAG | ACAGTGTTGG | 180 |
| AAGAAAGTAC | GGGGAAAAAC | GTGAAGATTC | AGAAGATAAA | GAAGAGAAGC | GTTATTATAC | 240 |
| GAACTATTAC | TTTAATCAAA | ATCATTCTTT | AGAGACAGGT | TGGCTTTATG | ATCAGTCTAA | 300 |
| CTGGTATTAT | CTAGCTAAGA | CGGAAATTAA | TGGAGAAAAC | TACCTTGGTG | GTGAAAGACG | 360 |

TGC GGGGTGG ATAAACGATG ATTCGACTTG GTACTACCTA GATCCAACAA CTGGTATTAT 420
 GCAAACAGGT TGGCAATATC TAGGTAATAA GTGGTACTAC CTCCGTTCTT CAGGAGCAAT 480
 GGCCACTGGC TGGTATCAGG AAGGTACCAC TTGGTATTAT TTAGACCACC CAAATGGCGA 540
 TATGAAAACA GGTGCGCAA ACCTGGGAA CAAATGGTAC TATCTCCGTT CATCAGGAGC 600
 TATGGCAACT GGTGTTATC AAGATGGTTC AACTTGGTAC TACCTAAATG CAGGTAATGG 660
 AGACATGAAG ACAGGTTGGT TCCAGGTCAA TGGCAACTGG TACTATGCTT ATAGCTCAGG 720
 TGCTTTGGCA GTGAATACGA CCGTAGATGG CTATTCTGTC AACTATAATG GCGAATGGGT 780
 TCGG 784

(2) INFORMATION FOR SEQ ID NO:152:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 261 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:152:

Val	Val	Gly	Trp	Gln	Tyr	Ile	Pro	Phe	Pro	Ser	Lys	Gly	Ser	Thr	Ile	1	5	10	15
Gly	Pro	Tyr	Pro	Asn	Gly	Ile	Arg	Leu	Glu	Gly	Phe	Pro	Lys	Ser	Glu	20	25	30	
Trp	Tyr	Tyr	Phe	Asp	Lys	Asn	Gly	Val	Leu	Gln	Glu	Phe	Val	Gly	Trp	35	40	45	
Lys	Thr	Leu	Glu	Ile	Lys	Thr	Lys	Asp	Ser	Val	Gly	Arg	Lys	Tyr	Gly	50	55	60	
Glu	Lys	Arg	Glu	Asp	Ser	Glu	Asp	Lys	Glu	Glu	Lys	Arg	Tyr	Tyr	Thr	65	70	75	80
Asn	Tyr	Tyr	Phe	Asn	Gln	Asn	His	Ser	Leu	Glu	Thr	Gly	Trp	Leu	Tyr	85	90	95	
Asp	Gln	Ser	Asn	Trp	Tyr	Tyr	Leu	Ala	Lys	Thr	Glu	Ile	Asn	Gly	Glu	100	105	110	
Asn	Tyr	Leu	Gly	Gly	Glu	Arg	Arg	Ala	Gly	Trp	Ile	Asn	Asp	Asp	Ser	115	120	125	
Thr	Trp	Tyr	Tyr	Leu	Asp	Pro	Thr	Thr	Gly	Ile	Met	Gln	Thr	Gly	Trp	130	135	140	
Gln	Tyr	Leu	Gly	Asn	Lys	Trp	Tyr	Tyr	Leu	Arg	Ser	Ser	Gly	Ala	Met	145	150	155	160
Ala	Thr	Gly	Trp	Tyr	Gln	Glu	Gly	Thr	Thr	Trp	Tyr	Tyr	Leu	Asp	His	165	170	175	
Pro	Asn	Gly	Asp	Met	Lys	Thr	Gly	Trp	Gln	Asn	Leu	Gly	Asn	Lys	Trp				

260

180

185

190

Tyr Tyr Leu Arg Ser Ser Gly Ala Met Ala Thr Gly Trp Tyr Gln Asp
195 200 205

Gly Ser Thr Trp Tyr Tyr Leu Asn Ala Gly Asn Gly Asp Met Lys Thr
210 215 220

Gly Trp Phe Gln Val Asn Gly Asn Trp Tyr Tyr Ala Tyr Ser Ser Gly
225 230 235 240

Ala Leu Ala Val Asn Thr Thr Val Asp Gly Tyr Ser Val Asn Tyr Asn
245 250 255

Gly Glu Trp Val Arg
260

(2) INFORMATION FOR SEQ ID NO: 153:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1708 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 153:

GGCCAAATCA GAATGGGTAG AAGACAAGGG AGCCTTTTAT TATCTTGACC AAGATGGAAA	60
GATGAAAAGA AATGCTTGGG TAGGAACTTC CTATGTTGGT GCAACAGGTG CCAAAGTAAT	120
AGAAGACTGG GTCTATGATT CTCAATACGA TGCTTGTTTT TATATCAAAG CAGATGGACA	180
GCACGCAGAG AAAGAATGGC TCCAAATTAA AGGGAAGGAC TATTATTTCA AATCCGGTGG	240
TTATCTACTG ACAAGTCAGT GGATTAATCA AGCTTATGTG AATGCTAGTG GTGCCAAAGT	300
ACAGCAAGGT TGGCTTTTTG ACAAACAATA CCAATCTTGG TTTTACATCA AAGAAAATGG	360
AAACTATGCT GATAAAGAAT GGATTTTCGA GAATGGTCAC TATTATTATC TAAATCCGG	420
TGGCTACATG GCAGCCAATG AATGGATTGG GGATAAGGAA TCTTGGTTTT ATCTCAAATT	480
TGATGGGAAA ATGGCTGAAA AAGAATGGGT CTACGATTCT CATAGTCAAG CTTGGTACTA	540
CTTCAAATCC GGTGGTTACA TGACAGCCAA TGAATGGATT TGGGATAAGG AATCTTGTTT	600
TTATCTCAAA TCTGATGGGA AAATAGCTGA AAAAGAATGG GTCTACGATT CTCATAGTCA	660
AGCTTGGTAC TACTTCAAAT CCGGTGGTTA CATGACAGCC AATGAATGGA TTTGGGATAA	720
GGAATCTTGG TTTTACCTCA AATCTGATGG GAAAATAGCT GAAAAAGAAT GGGTCTACGA	780
TTCTCATAGT CAAGCTTGGT ACTACTTCAA ATCTGGTGGC TACATGGCGA AAAATGAGAC	840
AGTAGATGGT TATCAGCTTG GAAGCGATGG TAAATGGCTT GGAGGAAAAA CTACAAATGA	900
AAATGCTGCT-TACTATCAAG TAGTGCCTGT TACAGCCAAT GTTTATGATT CAGATGGTGA	960
AAAGCTTTCC TATATATCGC AAGGTAGTGT CGTATGGCTA GATAAGGATA GAAAAAGTGA	1020

00524-0400 4259260

TGACAAGCGC TTGGCTATTA CTATTTCTGG TTTGTCAGGC TATATGAAAA CAGAAGATTT 1080
 ACAAGCGCTA GATGCTAGTA AGGACTTTAT CCCTTATTAT GAGAGTGATG GCCACCGTTT 1140
 TTATCACTAT GTGGCTCAGA ATGCTAGTAT CCCAGTAGCT TCTCATCTTT CTGATATGGA 1200
 AGTAGGCAAG AAATATTATT CGGCAGATGG CCTGCATTTT GATGGTTTTA AGCTTGAGAA 1260
 TCCCTTCCTT TTCAAAGATT TAACAGAGGC TACAAACTAC AGTGCTGAAG AATTGGATAA 1320
 GGTATTTAGT TTGCTAAACA TTAACAATAG CCTTTTGGAG AACAAGGGCG CTACTIONTTAA 1380
 GGAAGCCGAA GAACATTACC ATATCAATGC TCTTTATCTC CTTGCCCCATA GTGCCCTAGA 1440
 AAGTAACTGG GGAAGAAGTA AAATTGCCAA AGATAAGAAT AATTTCTTTG GCATTACAGC 1500
 CTATGATACG ACCCCTTACC TTTCTGCTAA GACATTTGAT GATGTGGATA AGGGAATTTT 1560
 AGGTGCAACC AAGTGGATTA AGGAAAATTA TATCGATAGG GGAAGAACTT TCCTTGAAAA 1620
 CAAGGCTTCT GGTATGAATG TGGAATATGC TTCAGACCCT TATTGGGGCG AAAAAATTGC 1680
 TAGTGTGATG ATGAAAATCA ATGAGAAG 1708

(2) INFORMATION FOR SEQ ID NO:154:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 569 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:154:

Ala Lys Ser Glu Trp Val Glu Asp Lys Gly Ala Phe Tyr Tyr Leu Asp
 1 5 10 15

Gln Asp Gly Lys Met Lys Arg Asn Ala Trp Val Gly Thr Ser Tyr Val
 20 25 30

Gly Ala Thr Gly Ala Lys Val Ile Glu Asp Trp Val Tyr Asp Ser Gln
 35 40 45

Tyr Asp Ala Trp Phe Tyr Ile Lys Ala Asp Gly Gln His Ala Glu Lys
 50 55 60

Glu Trp Leu Gln Ile Lys Gly Lys Asp Tyr Tyr Phe Lys Ser Gly Gly
 65 70 75 80

Tyr Leu Leu Thr Ser Gln Trp Ile Asn Gln Ala Tyr Val Asn Ala Ser
 85 90 95

Gly Ala Lys Val Gln Gln Gly Trp Leu Phe Asp Lys Gln Tyr Gln Ser
 100 105 110

Trp Phe Tyr Ile Lys Glu Asn Gly Asn Tyr Ala Asp Lys Glu Trp Ile
 115 120 125

Phe Glu Asn Gly His Tyr Tyr Tyr Leu Lys Ser Gly Gly Tyr Met Ala
 130 135 140

(2) INFORMATION FOR SEO ID NO: 155:

(A) LENGTH: 946 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

ATTTCGAGAT	GATTCTGAAG	GATGGCAGTT	TGTCCAAGAA	AATGGTAGAA	CCTACTACAA	60
AAAGGGGGAT	CTAAAAGAAA	CCTACTGGAG	AGTGATAGAT	GGGAAGTACT	ATTATTTTGA	120
TCCTTTATCC	GGAGAGATGG	TTGTCGGCTG	GCAATATATA	CCTGCTCCAC	ACAAGGGGGT	180
TACGATTGGT	CCTTCTCCAA	GAATAGAGAT	TGCTCTTAGA	CCAGATTGGT	TTTATTTTGG	240
TCAAGATGGT	GTATTACAAG	AATTTGTTGG	CAAGCAAGTT	TTAGAAGCAA	AAACTGCTAC	300
GAATACCAAC	AAACATCATG	GGGAAGAATA	TGATAGCCAA	GCAGAGAAAC	GAGTCTATTA	360
TTTTGAAGAT	CAGCGTAGTT	ATCATACTTT	AAAAACTGGT	TGGATTTATG	AAGAGGGTCA	420
TTGGTATTAT	TTACAGAAGG	ATGGTGGCTT	TGATTCGCGC	ATCAACAGAT	TGACGGTTGG	480
AGAGCTAGCA	CGTGGTTGGG	TTAAGGATTA	CCCTCTTACG	TATGATGAAG	AGAAGCTAAA	540
AGCAGCTCCA	TGGTACTATC	TAAATCCAGC	AACTGGCATT	ATGCAAACAG	GTTGGCAATA	600
TCTAGGTAAT	AGATGGTACT	ACCTCCATTC	GTCAGGAGCT	ATGGCAACTG	GCTGGTATAA	660
GGAAGGCTCA	ACTTGGTACT	ATCTAGATGC	TGAAAATGGT	GATATGAGAA	CTGGCTGGCA	720
AAACCTTGGG	AACAAATGGT	ACTATCTCCG	TTCATCAGGA	GCTATGGCAA	CTGGTTGGTA	780
TCAGGAAAGT	TCGACTTGGT	ACTATCTAAA	TGCAAGTAAT	GGAGATATGA	AAACAGGCTG	840
GTTCCAAGTC	AATGGTAACT	GGTACTATGC	CTATGATTCA	GGTGCTTTAG	CTGTTAATAC	900
CACAGTAGGT	GGTTACTACT	TAAACTATAA	TGGTGAATGG	GTTAAG		946

(2) INFORMATION FOR SEQ ID NO:156:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 316 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:156:

Val	Phe	Ala	Asp	Asp	Ser	Glu	Gly	Trp	Gln	Phe	Val	Gln	Glu	Asn	Gly	1	5	10	15
Arg	Thr	Tyr	Tyr	Lys	Lys	Gly	Asp	Leu	Lys	Glu	Thr	Tyr	Trp	Arg	Val	20	25	30	
Ile	Asp	Gly	Lys	Tyr	Tyr	Tyr	Phe	Asp	Pro	Leu	Ser	Gly	Glu	Met	Val	35	40	45	
Val	Gly	Trp	Gln	Tyr	Ile	Pro	Ala	Pro	His	Lys	Gly	Val	Thr	Ile	Gly	50	55	60	
Pro	Ser	Pro	Arg	Ile	Glu	Ile	Ala	Leu	Arg	Pro	Asp	Trp	Phe	Tyr	Phe	65	70	75	80
Gly	Gln	Asp	Gly	Val	Leu	Gln	Glu	Phe	Val	Gly	Lys	Gln	Val	Leu	Glu	85	90	95	
Ala	Lys	Thr	Ala	Thr	Asn	Thr	Asn	Lys	His	His	Gly	Glu	Glu	Tyr	Asp	100	105	110	
Ser	Gln	Ala	Glu	Lys	Arg	Val	Tyr	Tyr	Phe	Glu	Asp	Gln	Arg	Ser	Tyr	115	120	125	
His	Thr	Leu	Lys	Thr	Gly	Trp	Ile	Tyr	Glu	Glu	Gly	His	Trp	Tyr	Tyr	130	135	140	
Leu	Gln	Lys	Asp	Gly	Gly	Phe	Asp	Ser	Arg	Ile	Asn	Arg	Leu	Thr	Val	145	150	155	160
Gly	Glu	Leu	Ala	Arg	Gly	Trp	Val	Lys	Asp	Tyr	Pro	Leu	Thr	Tyr	Asp	165	170	175	
Glu	Glu	Lys	Leu	Lys	Ala	Ala	Pro	Trp	Tyr	Tyr	Leu	Asn	Pro	Ala	Thr	180	185	190	
Gly	Ile	Met	Gln	Thr	Gly	Trp	Gln	Tyr	Leu	Gly	Asn	Arg	Trp	Tyr	Tyr	195	200	205	
Leu	His	Ser	Ser	Gly	Ala	Met	Ala	Thr	Gly	Trp	Tyr	Lys	Glu	Gly	Ser	210	215	220	
Thr	Trp	Tyr	Tyr	Leu	Asp	Ala	Glu	Asn	Gly	Asp	Met	Arg	Thr	Gly	Trp	225	230	235	240
Gln	Asn	Leu	Gly	Asn	Lys	Trp	Tyr	Tyr	Leu	Arg	Ser	Ser	Gly	Ala	Met	245	250	255	
Ala	Thr	Gly	Trp	Tyr	Gln	Glu	Ser	Ser	Thr	Trp	Tyr	Tyr	Leu	Asn	Ala	260	265	270	

(2) INFORMATION FOR SEQ ID NO: 157:

(A) LENGTH: 1415 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

TGTCGCTGCA	AATGAAACTG	AAGTAGCAAA	AAC TTCG CAG	GATACAACGA	CAGCTTCAAG	60
TAGTTCAGAG	CAAAATCAGT	CTTCTAATAA	AACGCAAACG	AGCGCAGAAG	TACAGACTAA	120
TGCTGCTGCC	CACTGGGATG	GGGATTATTA	TGTAAAGGAT	GATGGTTCTA	AAGCTCAAAG	180
TGAATGGATT	TTTGACAAC T	ACTATAAGGC	TTGGTTTTAT	ATTAATTCAG	ATGGTCGTTA	240
CTCGCAGAAT	GAATGGCATG	GAAATTACTA	CCTGAAATCA	GGTGGATATA	TGGCCCCAAA	300
CGAGTGGATC	TATGACAGTA	ATTACAAGAG	TTGGTTTTAT	CTCAAGTCAG	ATGGGGCTTA	360
TGCTCATCAA	GAATGGCAAT	TGATTGGAAA	TAAGTGGTAC	TACTTCAAGA	AGTGGGGTTA	420
CATGGCTAAA	AGCCAATGGC	AAGGAAGTTA	TTTCTTGAAT	GGTCAAGGAG	CTATGATGCA	480
AAATGAATGG	CTSCTATGAT	CCAGCCTATT	CTGCTTATTT	TTATCTAAAA	TCCGATGGAA	540
CTTATGCTAA	CCAAGAGTGG	CAAAAAGTGG	GCGGCAAATG	GTACTATTTT	AAGAAGTGGG	600
GCTATATGGC	TCGGAATGAG	TGGCAAGGCA	ACTACTATTT	GACTGGAAAGT	GGTGCCATGG	660
CGACTGACGA	AGTGATTATG	GATGGTACTC	GCTATATCTT	TGCGGCCTCT	GGTGAGCTCA	720
AAGAAA AAAA	AGATTTGAAT	GTCGGCTGGG	TTACAGAGA	TGGTAAGCGC	TATTTCTTTA	780
ATAATAGAGA	AGAACAAGTG	GGAACCGAAC	ATGCTAAGAA	AGTCATTGAT	ATTAGTGAGC	840
ACAATGGTCG	TATCAATGAT	TGGAAAAAGG	TTATTGATGA	GAACGAAGTG	GATGGTGTCA	900
TTGTTCTGCT	AGGTTATAGC	GGTAAAGAAG	ACAAGGAATT	GGCGCATAAC	ATTAAGGAGT	960
TAAACCGTCT	GGGAATTCCT	TATGGTGTCT	ATCTCTATAC	CTATGCTGAA	AATGAGACCG	1020
ATGCTGAGAG	TGACGCTAAA	CAGACCATTG	AAC TTATAAA	GAAATACAAT	ATGAACCTGT	1080
CTTACCC TAT	CTATTATGAT	GTTGAGAATT	GGGAATATGT	AAATAAGAGC	AAGAGAGCTC	1140
CAAGTGATAC	AGGCACTTGG	GTTAAAATCA	TCAACAAGTA	CATGGACACG	ATGAAGCAGG	1200
CGGGTTTATCA	AAATGTGTAT	GTCTATAGCT	ATCGTAGTTT	ATTACAGACG	CGTTTAAAAAC	1260

ACCCAGATAT TTTAAACAT GTAAACTGGG TAGCGGCCTA TACGAATGCT TTAGAATGGG 1320
 AAAACCCTCA TTATTCAGGA AAAAAAGGTT GGCAATATAC CTCTTCTGAA TACATGAAAG 1380
 GAATCCAAGG GCGCGTAGAT GTCAGCGTTT GGTAT 1415

(2) INFORMATION FOR SEQ ID NO:158:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 471 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:158:

Val	Ala	Ala	Asn	Glu	Thr	Glu	Val	Ala	Lys	Thr	Ser	Gln	Asp	Thr	Thr	1	5	10	15
Thr	Ala	Ser	Ser	Ser	Glu	Gln	Asn	Gln	Ser	Ser	Asn	Lys	Thr	Gln		20	25	30	
Thr	Ser	Ala	Glu	Val	Gln	Thr	Asn	Ala	Ala	Ala	His	Trp	Asp	Gly	Asp	35	40	45	
Tyr	Tyr	Val	Lys	Asp	Asp	Gly	Ser	Lys	Ala	Gln	Ser	Glu	Trp	Ile	Phe	50	55	60	
Asp	Asn	Tyr	Tyr	Lys	Ala	Trp	Phe	Tyr	Ile	Asn	Ser	Asp	Gly	Arg	Tyr	65	70	75	80
Ser	Gln	Asn	Glu	Trp	His	Gly	Asn	Tyr	Tyr	Leu	Lys	Ser	Gly	Gly	Tyr	85	90	95	
Met	Ala	Gln	Asn	Glu	Trp	Ile	Tyr	Asp	Ser	Asn	Tyr	Lys	Ser	Trp	Phe	100	105	110	
Tyr	Leu	Lys	Ser	Asp	Gly	Ala	Tyr	Ala	His	Gln	Glu	Trp	Gln	Leu	Ile	115	120	125	
Gly	Asn	Lys	Trp	Tyr	Tyr	Phe	Lys	Lys	Trp	Gly	Tyr	Met	Ala	Lys	Ser	130	135	140	
Gln	Trp	Gln	Gly	Ser	Tyr	Phe	Leu	Asn	Gly	Gln	Gly	Ala	Met	Met	Gln	145	150	155	160
Asn	Glu	Trp	Leu	Tyr	Asp	Pro	Ala	Tyr	Ser	Ala	Tyr	Phe	Tyr	Leu	Lys	165	170	175	
Ser	Asp	Gly	Thr	Tyr	Ala	Asn	Gln	Glu	Trp	Gln	Lys	Val	Gly	Gly	Lys	180	185	190	
Trp	Tyr	Tyr	Phe	Lys	Lys	Trp	Gly	Tyr	Met	Ala	Arg	Asn	Glu	Trp	Gln	195	200	205	
Gly	Asn	Tyr	Tyr	Leu	Thr	Gly	Ser	Gly	Ala	Met	Ala	Thr	Asp	Glu	Val	210	215	220	
Ile	Met	Asp	Gly	Thr	Arg	Tyr	Ile	Phe	Ala	Ala	Ser	Gly	Glu	Leu	Lys				

267

225		230		235		240
Glu Lys Lys Asp	Leu Asn Val Gly Trp	Val His Arg Asp	Gly Lys Arg			
	245		250		255	
Tyr Phe Phe Asn	Asn Arg Glu Glu Gln	Val Gly Thr Glu	His Ala Lys			
	260		265		270	
Lys Val Ile Asp	Ile Ser Glu His Asn	Gly Arg Ile Asn	Asp Trp Lys			
	275		280		285	
Lys Val Ile Asp	Glu Asn Glu Val Asp	Gly Val Ile Val	Arg Leu Gly			
	290		295		300	
Tyr Ser Gly Lys	Glu Asp Lys Glu Leu	Ala His Asn Ile	Lys Glu Leu			
	305		310		315	320
Asn Arg Leu Gly	Ile Pro Tyr Gly	Val Tyr Leu Tyr	Thr Tyr Ala Glu			
	325		330		335	
Asn Glu Thr Asp	Ala Glu Ser Asp	Ala Lys Gln Thr	Ile Glu Leu Ile			
	340		345		350	
Lys Lys Tyr Asn	Met Asn Leu Ser	Tyr Pro Ile Tyr	Tyr Asp Val Glu			
	355		360		365	
Asn Trp Glu Tyr	Val Asn Lys Ser	Lys Arg Ala Pro	Ser Asp Thr Gly			
	370		375		380	
Thr Trp Val Lys	Ile Ile Asn Lys	Tyr Met Asp Thr	Met Lys Gln Ala			
	385		390		395	400
Gly Tyr Gln Asn	Val Tyr Val Tyr	Ser Tyr Arg Ser	Leu Leu Gln Thr			
	405		410		415	
Arg Leu Lys His	Pro Asp Ile Leu	Lys His Val Asn	Trp Val Ala Ala			
	420		425		430	
Tyr Thr Asn Ala	Leu Glu Trp Glu	Asn Pro His Tyr	Ser Gly Lys Lys			
	435		440		445	
Gly Trp Gln Tyr	Thr Ser Ser Glu	Tyr Met Lys Gly	Ile Gln Gly Arg			
	450		455		460	
Val Asp Val Ser	Val Trp Tyr					
	465		470			

(2) INFORMATION FOR SEQ ID NO: 159:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1924 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 159:

TACGTCTCAG CCTACTTTTG TAAGAGCAGA AGAATCTCCA CAAGTTGTCG AAAAATCTTC	60
ATTAGAGAAG AAATATGAGG AAGCAAAGC AAAAGCTGAT ACTGCCAAGA AAGATTACGA	120

AACGGCTAAA	AAGAAAGCAG	AAGACGCTCA	GAAAAAGTAT	GAAGATGATC	AGAAGAGAAC	180
TGAGGAGAAA	GCTCGAAAAG	AAGCAGAAGC	ATCTCAAAAA	TTGAATGATG	TGGCGCTTGT	240
TGTTCAAAAT	GCATATAAAG	AGTACCGAGA	AGTTCAAAAT	CAACGTAGTA	AATATAAATC	300
TGACGCTGAA	TATCAGAAAA	AATTAACAGA	GGTCGACTCT	AAAATAGAGA	AGGCTAGGAA	360
AGAGCAACAG	GACTTGCAAA	ATAAATTTAA	TGAAGTAAGA	GCAGTTGTAG	TTCCTGAACC	420
AAATGCGTTG	GCTGAGACTA	AGAAAAAAGC	AGAAGAAGCT	AAAGCAGAAG	AAAAAGTAGC	480
TAAGAGAAAA	TATGATTATG	CAACTCTAAA	GGTAGCACTA	GCGAAGAAAG	AAGTAGAGGC	540
TAAGGAACCT	GAAATTGAAA	AACCTCAATA	TGAAATTTCT	ACTTTGGAAC	AAGAAGTTGC	600
TACTGCTCAA	CATCAAGTAG	ATAATTTGAA	AAAACCTCTT	GCTGGTGCGG	ATCCTGATGA	660
TGGCACAGAA	GTTATAGAAG	CTAAATTAAA	AAAAGGAGAA	GCTGAGCTAA	ACGCTAAACA	720
AGCTGAGTTA	GCAAAAAAAC	AAACAGAACT	TGAAAAACTT	CTTGACAGCC	TTGATCCTGA	780
AGGTAAGACT	CAGGATGAAT	TAGATAAAGA	AGCAGAAGAA	GCTGAGTTGG	ATAAAAAAGC	840
TGATGAACTT	CAAATAAAG	TTGCTGATTT	AGAAAAAGAA	ATTAGTAACC	TTGAAATATT	900
ACTTGGAGGG	GCTGATNCTG	AAGATGATAC	TGCTGCTCTT	CAAATAAAT	TAGCTACTAA	960
AAAAGCTGAA	TTGGAAAAAA	CTCAAAAAGA	ATTAGATGCA	GCTCTTAATG	AGTTAGGCC	1020
TGATGGAGAT	GAAGAAGAAA	CTCCAGCGCC	GGCTCCTCAA	CCAGAGCAAC	CAGCTCCTGC	1080
ACCAAAACCA	GAGCAACCAG	CTCCAGCTCC	AAAACCAGAG	CAACCAGCTC	CTGCACCAAA	1140
ACCAGAGCAA	CCAGCTCCAG	CTCCAAAACC	AGAGCAACCA	GCTCCAGCTC	CAAAACCAGA	1200
GCAACCAGCT	AAGCCGGAGA	AACCAGCTGA	AGAGCCTACT	CAACCAGAAA	AACCAGCCAC	1260
TCCAAAAACA	GGCTGGAAAC	AAGAAAACGG	TATGTGGTAT	TTCTACAATA	CTGATGGTTC	1320
AATGGCAATA	GGTTGGCTCC	AAAACAACGG	TTCATGGTAC	TACCTAAACG	CTAACGGCGC	1380
TATGGCAACA	GGTTGGGTGA	AAGATGGAGA	TACCTGGTAC	TATCTTGAAG	CATCAGGTGC	1440
TATGAAAGCA	AGCCAATGGT	TCAAAGTATC	AGATAAATGG	TACTATGTCA	ACAGCAATGG	1500
CGCTATGGCG	ACAGGCTGGC	TCCAATACAA	TGGCTCATGG	TACTACCTCA	ACGCTAATGG	1560
TGATATGGCG	ACAGGATGGC	TCCAATACAA	CGGTTCATGG	TATTACCTCA	ACGCTAATGG	1620
TGATATGGCG	ACAGGATGGG	CTAAAGTCAA	CGGTTCATGG	TACTACCTAA	ACGCTAACGG	1680
TGCTATGGCT	ACAGGTTGGG	CTAAAGTCAA	CGGTTCATGG	TACTACCTAA	ACGCTAACGG	1740
TTCAATGGCA	ACAGGTTGGG	TGAAAGATGG	AGATACCTGG	TACTATCTTG	AAGCATCAGG	1800
TGCTATGAAA	GCAAGCCAAT	GGTTCAAAGT	ATCAGATAAA	TGGTACTATG	TCAATGGCTT	1860
AGGTGCCCTT	GCAGTCAACA	CAACTGTAGA	TGGCTATAAA	GTCAATGCCA	ATGGTGAATG	1920
GGTT						1924

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 641 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:160:

Thr	Ser	Gln	Pro	Thr	Phe	Val	Arg	Ala	Glu	Glu	Ser	Pro	Gln	Val	Val	1	5	10	15
Glu	Lys	Ser	Ser	Leu	Glu	Lys	Lys	Tyr	Glu	Glu	Ala	Lys	Ala	Lys	Ala	20	25	30	
Asp	Thr	Ala	Lys	Lys	Asp	Tyr	Glu	Thr	Ala	Lys	Lys	Lys	Ala	Glu	Asp	35	40	45	
Ala	Gln	Lys	Lys	Tyr	Glu	Asp	Asp	Gln	Lys	Arg	Thr	Glu	Glu	Lys	Ala	50	55	60	
Arg	Lys	Glu	Ala	Glu	Ala	Ser	Gln	Lys	Leu	Asn	Asp	Val	Ala	Leu	Val	65	70	75	80
Val	Gln	Asn	Ala	Tyr	Lys	Glu	Tyr	Arg	Glu	Val	Gln	Asn	Gln	Arg	Ser	85	90	95	
Lys	Tyr	Lys	Ser	Asp	Ala	Glu	Tyr	Gln	Lys	Lys	Leu	Thr	Glu	Val	Asp	100	105	110	
Ser	Lys	Ile	Glu	Lys	Ala	Arg	Lys	Glu	Gln	Gln	Asp	Leu	Gln	Asn	Lys	115	120	125	
Phe	Asn	Glu	Val	Arg	Ala	Val	Val	Val	Pro	Glu	Pro	Asn	Ala	Leu	Ala	130	135	140	
Glu	Thr	Lys	Lys	Lys	Ala	Glu	Glu	Ala	Lys	Ala	Glu	Glu	Lys	Val	Ala	145	150	155	160
Lys	Arg	Lys	Tyr	Asp	Tyr	Ala	Thr	Leu	Lys	Val	Ala	Leu	Ala	Lys	Lys	165	170	175	
Glu	Val	Glu	Ala	Lys	Glu	Leu	Glu	Ile	Glu	Lys	Leu	Gln	Tyr	Glu	Ile	180	185	190	
Ser	Thr	Leu	Glu	Gln	Glu	Val	Ala	Thr	Ala	Gln	His	Gln	Val	Asp	Asn	195	200	205	
Leu	Lys	Lys	Leu	Leu	Ala	Gly	Ala	Asp	Pro	Asp	Asp	Gly	Thr	Glu	Val	210	215	220	
Ile	Glu	Ala	Lys	Leu	Lys	Lys	Gly	Glu	Ala	Glu	Leu	Asn	Ala	Lys	Gln	225	230	235	240
Ala	Glu	Leu	Ala	Lys	Lys	Gln	Thr	Glu	Leu	Glu	Lys	Leu	Leu	Asp	Ser	245	250	255	
Leu	Asp	Pro	Glu	Gly	Lys	Thr	Gln	Asp	Glu	Leu	Asp	Lys	Glu	Ala	Glu	260	265	270	

T02210:1233260

Glu	Ala	Glu	Leu	Asp	Lys	Lys	Ala	Asp	Glu	Leu	Gln	Asn	Lys	Val	Ala		
		275					280					285					
Asp	Leu	Glu	Lys	Glu	Ile	Ser	Asn	Leu	Glu	Ile	Leu	Leu	Gly	Gly	Ala		
	290					295					300						
Asp	Xaa	Glu	Asp	Asp	Thr	Ala	Ala	Leu	Gln	Asn	Lys	Leu	Ala	Thr	Lys		
	305				310					315					320		
Lys	Ala	Glu	Leu	Glu	Lys	Thr	Gln	Lys	Glu	Leu	Asp	Ala	Ala	Leu	Asn		
				325					330					335			
Glu	Leu	Gly	Pro	Asp	Gly	Asp	Glu	Glu	Glu	Thr	Pro	Ala	Pro	Ala	Pro		
			340					345						350			
Gln	Pro	Glu	Gln	Pro	Ala	Pro	Ala	Pro	Lys	Pro	Glu	Gln	Pro	Ala	Pro		
		355					360					365					
Ala	Pro	Lys	Pro	Glu	Gln	Pro	Ala	Pro	Ala	Pro	Lys	Pro	Glu	Gln	Pro		
	370					375					380						
Ala	Pro	Ala	Pro	Lys	Pro	Glu	Gln	Pro	Ala	Pro	Ala	Pro	Lys	Pro	Glu		
	385					390					395						
Gln	Pro	Ala	Lys	Pro	Glu	Lys	Pro	Ala	Glu	Glu	Pro	Thr	Gln	Pro	Glu		
				405					410					415			
Lys	Pro	Ala	Thr	Pro	Lys	Thr	Gly	Trp	Lys	Gln	Glu	Asn	Gly	Met	Trp		
			420					425					430				
Tyr	Phe	Tyr	Asn	Thr	Asp	Gly	Ser	Met	Ala	Ile	Gly	Trp	Leu	Gln	Asn		
		435					440					445					
Asn	Gly	Ser	Trp	Tyr	Tyr	Leu	Asn	Ala	Asn	Gly	Ala	Met	Ala	Thr	Gly		
	450					455					460						
Trp	Val	Lys	Asp	Gly	Asp	Thr	Trp	Tyr	Tyr	Leu	Glu	Ala	Ser	Gly	Ala		
	465				470					475					480		
Met	Lys	Ala	Ser	Gln	Trp	Phe	Lys	Val	Ser	Asp	Lys	Trp	Tyr	Tyr	Val		
			485						490					495			
Asn	Ser	Asn	Gly	Ala	Met	Ala	Thr	Gly	Trp	Leu	Gln	Tyr	Asn	Gly	Ser		
			500					505					510				
Trp	Tyr	Tyr	Leu	Asn	Ala	Asn	Gly	Asp	Met	Ala	Thr	Gly	Trp	Leu	Gln		
		515					520					525					
Tyr	Asn	Gly	Ser	Trp	Tyr	Tyr	Leu	Asn	Ala	Asn	Gly	Asp	Met	Ala	Thr		
	530					535						540					
Gly	Trp	Ala	Lys	Val	Asn	Gly	Ser	Trp	Tyr	Tyr	Leu	Asn	Ala	Asn	Gly		
	545				550					555					560		
Ala	Met	Ala	Thr	Gly	Trp	Ala	Lys	Val	Asn	Gly	Ser	Trp	Tyr	Tyr	Leu		
			565						570					575			
Asn	Ala	Asn	Gly	Ser	Met	Ala	Thr	Gly	Trp	Val	Lys	Asp	Gly	Asp	Thr		
			580					585					590				
Trp	Tyr	Tyr	Leu	Glu	Ala	Ser	Gly	Ala	Met	Lys	Ala	Ser	Gln	Trp	Phe		
		595					600					605					

Lys Val Ser Asp Lys Trp Tyr Tyr Val Asn Gly Leu Gly Ala Leu Ala
 610 615 620

Val Asn Thr Thr Val Asp Gly Tyr Lys Val Asn Ala Asn Gly Glu Trp
 625 630 635 640

Val

(2) INFORMATION FOR SEQ ID NO: 161:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 670 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 161:

TGGACAGGTG AAAGGTCATG CTACATTTGT GAAATCCATG ACAACTGAAA TGTACCAAGA 60
 ACAACAGAAC CATTCTCTCG CCTACAATCA ACGCTTGGNT TCGCAAAATC GCATTGTAGA 120
 TCCTTTTTTTG GCGGAGGGAT ATGAGGTCAA TTACCAAGTG TCTGACGACC CTGATGCAGT 180
 CTATGGTTAC TTGTCTATTC CAAGTTTGA AATCATGGAG CCGGTTTATT TGGGAGCAGA 240
 TTATCATCAT TTAGGGATGG GCTTGGCTCA TGTGGATGGT ACACCGCTGC CTCTGGATGG 300
 TACAGGGATT CGCTCAGTGA TTGCTGGGCA CCGTGCAGAG CCAAGCCATG TCTTTTTCCG 360
 CCATTTGGAT CAGCTAAAAG TTGGAGATGC TCTTTATTAT GATAATGGCC AGGAAATTGT 420
 AGAATATCAG ATGATGGACA CAGAGATTAT TTTACCGTCG GAATGGGAAA AATTAGAATC 480
 GGTTAGCTCT AAAAATATCA TGACCTTGAT AACCTGCGAT CCGATTCTTA CCTTTAATAA 540
 ACGCTTATTA GTGAATTTTG AACGAGTCGC TGTTTATCAA AAATCAGATC CACAAACAGC 600
 TGCAGTTGCG AGGGTTGCTT TTACGAAAGA AGGACAATCT GTATCGCGTG TTGCAACCTC 660
 TCAATGGTTG 670

(2) INFORMATION FOR SEQ ID NO:162:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 223 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:162:

Gly Gln Val Lys Gly His Ala Thr Phe Val Lys Ser Met Thr Thr Glu
 1 5 10 15
 Met Tyr Gln Glu Gln Gln Asn His Ser Leu Ala Tyr Asn Gln Arg Leu
 20 25 30

(2) INFORMATION FOR SEQ ID NO: 163:

(A) LENGTH: 784 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

GATTGCTCCT	TTGAAGGATT	TGAGAGAAAC	CATGTTGGAA	ATTGCTTCTG	GTGCTCAAAA	60
TCTTCGTGCC	AAGGAAGTTG	GTGCCTATGA	ACTGAGAGAA	GTAAGTCGCC	AATTTAATGC	120
TATGTTGGAT	CAGATTGATC	AGTTGATGGT	AGCTATTTCGT	AGCCAGGAAG	AAACGACCCG	180
TCAGTACCAA	CTTCAAGCCC	TTTCGAGCCA	GATTAATCCA	CATTTCCCTCT	ATAACACTTT	240
GGACACCATC	ATCTGGATGG	CTGAATTTCA	TGATAGTCAG	CGAGTGGTGC	AGGTGACCAA	300
GTCCTTGGCA	ACCTATTTC	GCTTGGCGCT	CAATCAAGGC	AAGGACTTGA	TTTGTCTCTC	360
TGACGAAATC	AATCATGTCC	GCCAGTATCT	CTTTATCCAG	AAACAACGCT	ATGGAGATAA	420

GCTGGAATAC GAAATTAATG AAAATGTTGC CTTTGATAAT TTAGTCTTAC CCAAGCTGGT 480
 CCTACAACCC CTTGTAGAAA ATGCTCTTTA CCATGGCATT AAGGAAAAGG AAGGTCAGGG 540
 CCATATTAAA CTTTCTGTCC AGAAACAGGA TTCGGGATTG GTCATCCGTA TTGAGGATGA 600
 TGGCGTTGGC TTCCAAGATG CTGGTGATAG TAGTCAAAGT CAACTCAAAC GTGGGGGAGT 660
 TGGTCTTCAA AATGTCGATC AACGGCTCAA ACTTCATTTT GGAGCCAATT ACCATATGAA 720
 GATTGATTCT AGACCCCAAA AAGGGACGAA AGTTGAAATA TATATAAATA GAATAGAAAC 780
 TAGC 784

(2) INFORMATION FOR SEQ ID NO:164:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 261 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:164:

Ile Ala Pro Leu Lys Asp Leu Arg Glu Thr Met Leu Glu Ile Ala Ser
 1 5 10 15
 Gly Ala Gln Asn Leu Arg Ala Lys Glu Val Gly Ala Tyr Glu Leu Arg
 20 25 30
 Glu Val Thr Arg Gln Phe Asn Ala Met Leu Asp Gln Ile Asp Gln Leu
 35 40 45
 Met Val Ala Ile Arg Ser Gln Glu Glu Thr Thr Arg Gln Tyr Gln Leu
 50 55 60
 Gln Ala Leu Ser Ser Gln Ile Asn Pro His Phe Leu Tyr Asn Thr Leu
 65 70 75 80
 Asp Thr Ile Ile Trp Met Ala Glu Phe His Asp Ser Gln Arg Val Val
 85 90 95
 Gln Val Thr Lys Ser Leu Ala Thr Tyr Phe Arg Leu Ala Leu Asn Gln
 100 105 110
 Gly Lys Asp Leu Ile Cys Leu Ser Asp Glu Ile Asn His Val Arg Gln
 115 120 125
 Tyr Leu Phe Ile Gln Lys Gln Arg Tyr Gly Asp Lys Leu Glu Tyr Glu
 130 135 140
 Ile Asn Glu Asn Val Ala Phe Asp Asn Leu Val Leu Pro Lys Leu Val
 145 150 155 160
 Leu Gln Pro Leu Val Glu Asn Ala Leu Tyr His Gly Ile Lys Glu Lys
 165 170 175
 Glu Gly Gln Gly His Ile Lys Leu Ser Val Gln Lys Gln Asp Ser Gly
 180 185 190

Leu Val Ile Arg Ile Glu Asp Asp Gly Val Gly Phe Gln Asp Ala Gly
 195 200 205
 Asp Ser Ser Gln Ser Gln Leu Lys Arg Gly Gly Val Gly Leu Gln Asn
 210 215 220
 Val Asp Gln Arg Leu Lys Leu His Phe Gly Ala Asn Tyr His Met Lys
 225 230 235 240
 Ile Asp Ser Arg Pro Gln Lys Gly Thr Lys Val Glu Ile Tyr Ile Asn
 245 250 255
 Arg Ile Glu Thr Ser
 260

(2) INFORMATION FOR SEQ ID NO: 165:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 325 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 165:

TAGGTCATAT GGGACTTTTT TTCTACAACA AAATAGGCTC CATAATATCT ATAAGGGATT	60
TACCCACTAC AAATATTATA GAGCCGAAAA TTCACATCTA ATATATGCAG ACTACTTTGA	120
AATGAAATTA AAAAAATTAT TAAAGGATGA CACAAAAGTT TTTGAAAAAT CTACATTCAA	180
ATTTGTAGAA GGATATAAAA TATACCTGAC AGAATCTAAA GAATCTGGAA TTAAACAAAT	240
GGACAATGTC ATAAAATATT TTGAGTTTAT TGAATCTAAA AGTATTGCTT TATATTTTCA	300
AAAACGATTA AATGAGCTGA TAGAT	325

(2) INFORMATION FOR SEQ ID NO:166:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 108 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:166:

Arg Ser Tyr Gly Thr Phe Phe Leu Gln Gln Asn Arg Leu His Asn Ile	1 5 10 15
Tyr Lys Gly Phe Thr His Tyr Lys Tyr Tyr Arg Ala Glu Asn Ser His	20 25 30
Leu Ile Tyr Ala Asp Tyr Phe Glu Met Lys Leu Lys Lys Leu Leu Lys	35 40 45
Asp Asp Thr Lys Val Phe Glu Lys Ser Thr Phe Lys Phe Val Glu Gly	50 55 60

Tyr Lys Ile Tyr Leu Thr Glu Ser Lys Glu Ser Gly Ile Lys Gln Met
65 70 75 80

Asp Asn Val Ile Lys Tyr Phe Glu Phe Ile Glu Ser Lys Ser Ile Ala
85 90 95

Leu Tyr Phe Gln Lys Arg Leu Asn Glu Leu Ile Asp
100 105

(2) INFORMATION FOR SEQ ID NO: 167:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 238 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 167:

CAACGTTGAG AATTATTTGC GAATGTGTTT GGATAGCATT CAGAATCAGA CGTATCAAAA 60
 TTTTGAGTGT TTATTAATCA ATGATGGCTC TCCAGATCAT TCATCCAAAA TATGTGAAGA 120
 ATTTGTAGAG AAAGATTCTC GTTTCAAATA TTTTGAGAAA GCAAACGGCG GTCTTTCATC 180
 AGCTCGTAAC CTAGGTATTG AATGTTCTGGG GGGGGGCGTA CATTACTTTT GTAGACTC 238

(2) INFORMATION FOR SEQ ID NO:168:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 79 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:168:

Asn Val Glu Asn Tyr Leu Arg Met Cys Leu Asp Ser Ile Gln Asn Gln
1 5 10 15
 Thr Tyr Gln Asn Phe Glu Cys Leu Leu Ile Asn Asp Gly Ser Pro Asp
20 25 30
 His Ser Ser Lys Ile Cys Glu Glu Phe Val Glu Lys Asp Ser Arg Phe
35 40 45
 Lys Tyr Phe Glu Lys Ala Asn Gly Gly Leu Ser Ser Ala Arg Asn Leu
50 55 60
 Gly Ile Glu Cys Ser Gly Gly Gly Val His Tyr Phe Cys Arg Leu
65 70 75

(2) INFORMATION FOR SEQ ID NO: 169:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 742 base pairs
 (B) TYPE: nucleic acid

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 169:

(2) INFORMATION FOR SEQ ID NO:170:

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:170:

Tyr	Tyr	Gln	Ser	Ser	Ser	Ser	Ala	Ile	Glu	Ala	Thr	Ile	Glu	Gly	Asn
1				5					10					15	
Ser	Gln	Thr	Thr	Ile	Ser	Gln	Thr	Ser	His	Phe	Ile	Gln	Ser	Tyr	Ile
			20					25					30		
Lys	Lys	Leu	Glu	Thr	Thr	Ser	Thr	Gly	Leu	Thr	Gln	Gln	Thr	Asp	Val
		35					40					45			
Leu	Ala	Tyr	Ala	Glu	Asn	Pro	Ser	Gln	Asp	Lys	Val	Glu	Gly	Ile	Arg
	50					55					60				
Asp	Leu	Phe	Leu	Thr	Ile	Leu	Lys	Ser	Asp	Lys	Asp	Leu	Lys	Thr	Val
65					70					75				80	
Val	Leu	Val	Thr	Lys	Ser	Gly	Gln	Val	Ile	Ser	Thr	Asp	Asp	Ser	Val
				85					90					95	

Gln Met Lys Thr Ser Ser Asp Met Met Ala Glu Asp Trp Tyr Gln Lys
100 105 110

Ala Ile His Gln Gly Ala Met Pro Val Leu Thr Pro Ala Arg Lys Ser
115 120 125

Asp Ser Gln Trp Val Ile Ser Val Thr Gln Glu Leu Val Asp Ala Lys
130 135 140

Gly Ala Asn Leu Gly Val Leu Arg Leu Asp Ile Ser Tyr Glu Thr Leu
145 150 155 160

Glu Ala Tyr Leu Asn Gln Leu Gln Leu Gly Gln Gln Gly Phe Ala Phe
165 170 175

Ile Ile Asn Glu Asn His Glu Phe Val Tyr His Pro Gln His Thr Val
180 185 190

Tyr Ser Ser Ser Ser Lys Met Glu Ala Met Lys Pro Tyr Ile Asp Thr
195 200 205

Gly Gln Gly Tyr Thr Pro Gly His Lys Ser Tyr Val Ser Gln Glu Lys
210 215 220

Ile Ala Gly Thr Asp Trp Thr Val Leu Gly Val Ser Ser Leu Glu Lys
225 230 235 240

Leu Asp Gln Val Arg Ser Gln
245

(2) INFORMATION FOR SEQ ID NO: 171:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1282 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 171:

GACAAAAACA TTAAAACGTC CTGAGGTTTT ATCACCTGCA GGGACTTTAG AGAAGCTAAA	60
GGTAGCTGTT CAGTATGGAG CAGATGCTGT CTTTATCGGT GGTCAGGCCT ATGGTCTTCG	120
TAGCCGTGCG GGAAACTTTA CTTTCGAACA GATGGAAGAA GGC GTGCAGT TTGCGGCCAA	180
GTATGGTGCC AAGGTCTATG TAGCGGCTAA TATGGTTATG CACGAAGGAA ATGAAGCTGG	240
TGCTGGTGAG TGGTTCGGTA AACTGCGTGA TATCGGGATT GCAGCAGTTA TCGTATCTGA	300
CCCAGCCTTG ATTATGATTG CAGTGACTGA AGCACCAGGC CTTGAAATCC ACCTTTCTAC	360
CCAAGCCAGT GCCACTAACT ATGAAACCCT TGAGTTCTGG AAAGAGCTAG GCTTGACTCG	420
TGTCGTTTTA GCGCGTGAGG TTTCAATGGA AGAATTAGCT GAGATCCGCA AACGTACAGA	480
TGTTGAAATT GAAGCCTTTG TCCATGGAGC TATGTGTATT TCATACTCTG GACGTTGTAC	540
TCTTTCAAAC CACATGAGTA TGC GTGATGC CAACCGTGGT GGATGTTCTC AGTCATGCCG	600

TTGGAAATAC GACCTTTACG ATATGCCATT TGGGAAAGAA CGTAAGAGTT TGCAGGGTGA 660
 GATTCCAGAA GAATTTTCAA TGTCAGCCGT TGACATGTCT ATGATTGACC ANATTCCAGA 720
 TATGATTGAA AATGGTGTGG ACAGTCTAAA AATCGAAGGA CGTATGNAGT CTATTCACCTA 780
 NGTATCAACA GTAACCAACT GCTACAAGGC GGCTGTGGAT GCCTATCTTG AAAGTCCTGA 840
 AAAGTTTGAA GCTATCAAAC AAGACTTGGT GGACGAGATG TGAAGGTTG CCCAACGTGA 900
 ACTGGCTACA GGATTTTACT ATGGTACACC ATCTGAAAAT GAGCAGTTGT TTGGTGCTCG 960
 TCGTAAATC CCTGAGTACA AGTTTGTGCG TGAAGTGGTT TCTTATGATG ATGCGGCACA 1020
 AACAGCAACT ATTCGTCAAC GAAACGTCAT TAACGAAGGG GACCAAGTTG AGTTTTATGG 1080
 TCCAGGTTTC CGTCATTTTG AAACCTATAT TGAAGATTTG CATGATGCTA AAGGCAATAA 1140
 AATCGACCGC GCTCCAAATC CAATGGAACCT ATTGACTATT AAAGTCCCAC AACCTGTTCA 1200
 ATCAGGAGAC ATGGTTCGAG CTCTTAAAGA GGGGCTTATC AATCTTTATA AGGAAGATGG 1260
 AACCAGCGTC ACAGTTCGTG CT 1282

(2) INFORMATION FOR SEQ ID NO:172:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 427 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:172:

Thr Lys Thr Leu Lys Arg Pro Glu Val Leu Ser Pro Ala Gly Thr Leu
 1 5 10 15
 Glu Lys Leu Lys Val Ala Val Gln Tyr Gly Ala Asp Ala Val Phe Ile
 20 25 30
 Gly Gly Gln Ala Tyr Gly Leu Arg Ser Arg Ala Gly Asn Phe Thr Phe
 35 40 45
 Glu Gln Met Glu Glu Gly Val Gln Phe Ala Ala Lys Tyr Gly Ala Lys
 50 55 60
 Val Tyr Val Ala Ala Asn Met Val Met His Glu Gly Asn Glu Ala Gly
 65 70 75 80
 Ala Gly Glu Trp Phe Arg Lys Leu Arg Asp Ile Gly Ile Ala Ala Val
 85 90 95
 Ile Val Ser Asp Pro Ala Leu Ile Met Ile Ala Val Thr Glu Ala Pro
 100 105 110
 Gly Leu Glu Ile His Leu Ser Thr Gln Ala Ser Ala Thr Asn Tyr Glu
 115 120 125
 Thr Leu Glu Phe Trp Lys Glu Leu Gly Leu Thr Arg Val Val Leu Ala
 130 135 140

Arg Glu Val Ser Met Glu Glu Leu Ala Glu Ile Arg Lys Arg Thr Asp
 145 150 155 160
 Val Glu Ile Glu Ala Phe Val His Gly Ala Met Cys Ile Ser Tyr Ser
 165 170 175
 Gly Arg Cys Thr Leu Ser Asn His Met Ser Met Arg Asp Ala Asn Arg
 180 185 190
 Gly Gly Cys Ser Gln Ser Cys Arg Trp Lys Tyr Asp Leu Tyr Asp Met
 195 200 205
 Pro Phe Gly Lys Glu Arg Lys Ser Leu Gln Gly Glu Ile Pro Glu Glu
 210 215 220
 Phe Ser Met Ser Ala Val Asp Met Ser Met Ile Asp Xaa Ile Pro Asp
 225 230 235 240
 Met Ile Glu Asn Gly Val Asp Ser Leu Lys Ile Glu Gly Arg Met Xaa
 245 250 255
 Ser Ile His Xaa Val Ser Thr Val Thr Asn Cys Tyr Lys Ala Ala Val
 260 265 270
 Asp Ala Tyr Leu Glu Ser Pro Glu Lys Phe Glu Ala Ile Lys Gln Asp
 275 280 285
 Leu Val Asp Glu Met Trp Lys Val Ala Gln Arg Glu Leu Ala Thr Gly
 290 295 300
 Phe Tyr Tyr Gly Thr Pro Ser Glu Asn Glu Gln Leu Phe Gly Ala Arg
 305 310 315 320
 Arg Lys Ile Pro Glu Tyr Lys Phe Val Ala Glu Val Val Ser Tyr Asp
 325 330 335
 Asp Ala Ala Gln Thr Ala Thr Ile Arg Gln Arg Asn Val Ile Asn Glu
 340 345 350
 Gly Asp Gln Val Glu Phe Tyr Gly Pro Gly Phe Arg His Phe Glu Thr
 355 360 365
 Tyr Ile Glu Asp Leu His Asp Ala Lys Gly Asn Lys Ile Asp Arg Ala
 370 375 380
 Pro Asn Pro Met Glu Leu Leu Thr Ile Lys Val Pro Gln Pro Val Gln
 385 390 395 400
 Ser Gly Asp Met Val Arg Ala Leu Lys Glu Gly Leu Ile Asn Leu Tyr
 405 410 415
 Lys Glu Asp Gly Thr Ser Val Thr Val Arg Ala
 420 425

(2) INFORMATION FOR SEQ ID NO: 173:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 778 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 173:

TTCTCAGGAG ACCTTTAAAA ATATCACCAA TAGCTTCTCC ATGCAAATCA ATCGTCGCGT 60
 CAACCAAGGA ACGCCTCGTG GTGCTGGGAA TATCAAGGGT GAAGACATCA AAAAAATCAC 120
 CGAAAACAAG GCCATTGAGT CTTATGTCAA ACGTATCAAC GCTATCGGAG ATTTGACTGG 180
 ATATGACCTG ATTGAAACGC CAGAAACCAA GAAGAATCTC ACTGCTGATC GTGCCAAGCG 240
 TTTTGGAAGT AGCTTGATGA TTACAGGTGT CAATGACTCC TCTAAAGAAG ACAAGTTTGT 300
 CTCTGGTTCT TATAAACTAG TCGAAGGAGA GCACTTAACC AACGACGACA AGGATAAAAT 360
 CCTCTTGAC AAGGACTTGG CAGCCAAACA CGGCTGGAAA GTAGGGGACA AGGTAAACT 420
 GGACTCTAAT ATCTACGATG CAGATAATGA AAAAGGAGCC AAGGAAACAG TTGAAGTGAC 480
 AATCAAGGGA CTCTTTGATG GTCATAATAA GTCAGCAGTA ACCTACTCAC AAGAACTTTA 540
 CGAAAACACA GCTATTACAG ACATTCACAC TGCTGCAAAA CTTTATGGAT ACACAGAAGA 600
 CACAGCCATT TATGGGGACG CAACCTTCTT TGTAACAGCA GACAAGAACT TGGATGATGT 660
 TATGAAAGAG TTGAATGGCA TCAGTGGTAT CAACTGGAAG AGCTACACAC TCGTCAAGAG 720
 CTCCTCTAAC TACCCAGCTC TTGAGCAATC TATCTCTGGT ATGTACAAGA TGGCCAAC 778

(2) INFORMATION FOR SEQ ID NO:174:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 259 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:174:

Ser Gln Glu Thr Phe Lys Asn Ile Thr Asn Ser Phe Ser Met Gln Ile
 1 5 10 15
 Asn Arg Arg Val Asn Gln Gly Thr Pro Arg Gly Ala Gly Asn Ile Lys
 20 25 30
 Gly Glu Asp Ile Lys Lys Ile Thr Glu Asn Lys Ala Ile Glu Ser Tyr
 35 40 45
 Val Lys Arg Ile Asn Ala Ile Gly Asp Leu Thr Gly Tyr Asp Leu Ile
 50 55 60
 Glu Thr Pro Glu Thr Lys Lys Asn Leu Thr Ala Asp Arg Ala Lys Arg
 65 70 75 80
 Phe Gly Ser Ser Leu Met Ile Thr Gly Val Asn Asp Ser Ser Lys Glu
 85 90 95
 Asp Lys Phe Val Ser Gly Ser Tyr Lys Leu Val Glu Gly Glu His Leu
 100 105 110

Thr Asn Asp Asp Lys Asp Lys Ile Leu Leu His Lys Asp Leu Ala Ala
 115 120 125
 Lys His Gly Trp Lys Val Gly Asp Lys Val Lys Leu Asp Ser Asn Ile
 130 135 140
 Tyr Asp Ala Asp Asn Glu Lys Gly Ala Lys Glu Thr Val Glu Val Thr
 145 150 155 160
 Ile Lys Gly Leu Phe Asp Gly His Asn Lys Ser Ala Val Thr Tyr Ser
 165 170 175
 Gln Glu Leu Tyr Glu Asn Thr Ala Ile Thr Asp Ile His Thr Ala Ala
 180 185 190
 Lys Leu Tyr Gly Tyr Thr Glu Asp Thr Ala Ile Tyr Gly Asp Ala Thr
 195 200 205
 Phe Phe Val Thr Ala Asp Lys Asn Leu Asp Asp Val Met Lys Glu Leu
 210 215 220
 Asn Gly Ile Ser Gly Ile Asn Trp Lys Ser Tyr Thr Leu Val Lys Ser
 225 230 235 240
 Ser Ser Asn Tyr Pro Ala Leu Glu Gln Ser Ile Ser Gly Met Tyr Lys
 245 250 255
 Met Ala Asn

(2) INFORMATION FOR SEQ ID NO: 175:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 694 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 175:

AGTAAATGCG CAATCAAATT CATTAATATT AATAGATGAA CCTGAAATCT CACTTCATCC 60
 GAGTGCAATC TATAAATTTA AAGAGTTTTT ACTTCAAGAG TGTTTAAATA AAAACATCA 120
 AATTATTATC ACTACACATT CTACACAAC TATAAAAGAT TTTCTAGAG AAGCCGTGAA 180
 ACTTTTAGTG AAAACGGAG AAAAGGTAGA TGTTATTGAA AATATTGATT ATCAGGATGC 240
 ATTTTTTGAA TTAGGTGATG TGTATCATTC TAGGAAGATG ATTTATGTTG AAGATAGACT 300
 AGCTAAATAT ATTCTAGAGT TTGTTATCAC TCATTCAGGT AGTGAGAATC TTAAACAGAA 360
 TTTAGTAGTG AGATATATTC CTGGTGGAGC AAATCAAATA ATTTGTAATA ATATTTTAAA 420
 CTCATCGTAT TTAGATTCCG ATAACCATTA TTTTGGCTT GATGGAGATC AAAACACTAA 480
 TGTTAGTGAA TCAAATAATT TAATGAACTA TCTTGAAAT GGTGTTGTTA TATCAGATAA 540
 AATTCCTGAA TCAGATAATA AAAATCTTGA TGATATTATA AAATTGATAA NGGGATGTCC 600

AATTAAATTT AATGTTTCAG GTAATAAAGG GCAAAAAAAT AATATTGAAT TAATTGCGAA

660

ACAAAGAAGC TTTATAGATT ATTGGGCTAA ATAC

694

(2) INFORMATION FOR SEQ ID NO:176:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 231 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:176:

Val Asn Ala Gln Ser Asn Ser Leu Ile Leu Ile Asp Glu Pro Glu Ile
1 5 10 15

Ser Leu His Pro Ser Ala Ile Tyr Lys Phe Lys Glu Phe Leu Leu Gln
20 25 30

Glu Cys Leu Asn Lys Lys His Gln Ile Ile Ile Thr Thr His Ser Thr
35 40 45

Gln Leu Ile Lys Asp Phe Pro Arg Glu Ala Val Lys Leu Leu Val Lys
50 55 60

Asn Gly Glu Lys Val Asp Val Ile Glu Asn Ile Asp Tyr Gln Asp Ala
65 70 75 80

Phe Phe Glu Leu Gly Asp Val Tyr His Ser Arg Lys Met Ile Tyr Val
85 90 95

Glu Asp Arg Leu Ala Lys Tyr Ile Leu Glu Phe Val Ile Thr His Ser
100 105 110

Gly Ser Glu Asn Leu Lys Gln Asn Leu Val Val Arg Tyr Ile Pro Gly
115 120 125

Gly Ala Asn Gln Ile Ile Cys Asn Asn Ile Leu Asn Ser Ser Tyr Leu
130 135 140

Asp Ser Asp Asn His Tyr Phe Trp Leu Asp Gly Asp Gln Asn Thr Asn
145 150 155 160

Val Ser Glu Ser Asn Asn Leu Met Asn Tyr Leu Glu Asn Gly Val Val
165 170 175

Ile Ser Asp Lys Ile Pro Glu Ser Asp Asn Lys Asn Leu Asp Asp Ile
180 185 190

Ile Lys Leu Ile Xaa Gly Cys Pro Ile Lys Phe Asn Val Ser Gly Asn
195 200 205

Lys Gly Gln Lys Asn Asn Ile Glu Leu Ile Ala Lys Gln Arg Ser Phe
210 215 220

Ile Asp Tyr Trp Ala Lys Tyr
225 230

(2) INFORMATION FOR SEQ ID NO: 177:

0076934 04304

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 550 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 177:

TTACCGCGTT CATCAAGATG TCAAACAAGT CATGACCTAT CAACCCATGG TCGGAGAAAT 60
ATTGAGTGAA CAAGACACCC CAGCAAACGA AGAGCTTGTG CTTGCTATGA TTTATACTGA 120
AACAAAAGGA AAAGAAGGCG ATGTTATGCA GTCTAGTGAG TCTGCAAGTG GTTCCACCAA 180
CACCATCAAT GATAATGCCT CTAGCATTCTG GCAAGGCATT CAAACTCTGA CAGGCAATCT 240
CTATCTGGCG CAGAAGAAGG GGGTAGATAT CTGGACAGCT GTTCAAGCCT ATAATTTTGG 300
ACCTGCCTAT ATCGATTTTA TCGCCCAAAA TGGCAAGGAA AATACCCTGG CTCTAGCCAA 360
ACAGTACTCT CGTGAGACTG TTGCCCCCTT GCTTGGTAAT AGGACTGGAA AGACTTATAG 420
TTATATTAC CCCATTTCCTA TTTTTCACGG TGCTGAACTC TATGTAAATG GAGGAAACTA 480
TTATTATTCT AGACAGGTAC GACTTAACCT TTACATCATC AAATGTTTCA CTCTCTTTTC 540
AACATCTGGC 550

(2) INFORMATION FOR SEQ ID NO:178:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 183 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:178:

Tyr Arg Val His Gln Asp Val Lys Gln Val Met Thr Tyr Gln Pro Met
1 5 10 15
Val Arg Glu Ile Leu Ser Glu Gln Asp Thr Pro Ala Asn Glu Glu Leu
20 25 30
Val Leu Ala Met Ile Tyr Thr Glu Thr Lys Gly Lys Glu Gly Asp Val
35 40 45
Met Gln Ser Ser Glu Ser Ala Ser Gly Ser Thr Asn Thr Ile Asn Asp
50 55 60
Asn Ala Ser Ser Ile Arg Gln Gly Ile Gln Thr Leu Thr Gly Asn Leu
65 70 75 80
Tyr Leu Ala Gln Lys Lys Gly Val Asp Ile Trp Thr Ala Val Gln Ala
85 90 95
Tyr Asn Phe Gly Pro Ala Tyr Ile Asp Phe Ile Ala Gln Asn Gly Lys

284

100 105 110

Glu Asn Thr Leu Ala Leu Ala Lys Gln Tyr Ser Arg Glu Thr Val Ala
 115 120 125

Pro Leu Leu Gly Asn Arg Thr Gly Lys Thr Tyr Ser Tyr Ile His Pro
 130 135 140

Ile Ser Ile Phe His Gly Ala Glu Leu Tyr Val Asn Gly Gly Asn Tyr
 145 150 155 160

Tyr Tyr Ser Arg Gln Val Arg Leu Asn Leu Tyr Ile Ile Lys Cys Phe
 165 170 175

Thr Leu Phe Ser Thr Ser Gly
 180

(2) INFORMATION FOR SEQ ID NO: 179:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 334 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 179:

GTGGATGGGC TTAACTATC TTCGTATTCG CCGTGGGCT AAAATTGTGG ACAATGAGGA	60
GTTTGAAGCC TTGATTCGTA CGGGTCAATT GATTGATTG CGCGACCCAG CAGAATTCCA	120
CAGAAAACAT ATCCTTGGTG CACGCAATAT TCCTTCAAGT CAGTTGAAAA CTAGTCTTGC	180
AGCCCTTCGT AAAGATAAAC CTGTCCTTCT CTACGAAAAC CAACGTGCGC AACGAGTTAC	240
AAATGCAGCT CTTTACTTGA AAAACAAGG TTTTCTGAG ATTTATATCC TTTCTTATGG	300
CTTGGATTCT TGGAAAGGGA AAGTGAAGAC TAGC	334

(2) INFORMATION FOR SEQ ID NO:180:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 111 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:180:

Trp Met Gly Phe Asn Tyr Leu Arg Ile Arg Arg Ala Ala Lys Ile Val	
1 5 10 15	
Asp Asn Glu Glu Phe Glu Ala Leu Ile Arg Thr Gly Gln Leu Ile Asp	
20 25 30	
Leu Arg Asp Pro Ala Glu Phe His Arg Lys His Ile Leu Gly Ala Arg	
35 40 45	

Asn Ile Pro Ser Ser Gln Leu Lys Thr Ser Leu Ala Ala Leu Arg Lys
50 55 60

Asp Lys Pro Val Leu Leu Tyr Glu Asn Gln Arg Ala Gln Arg Val Thr
65 70 75 80

Asn Ala Ala Leu Tyr Leu Lys Lys Gln Gly Phe Ser Glu Ile Tyr Ile
85 90 95

Leu Ser Tyr Gly Leu Asp Ser Trp Lys Gly Lys Val Lys Thr Ser
100 105 110

(2) INFORMATION FOR SEQ ID NO: 181:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1342 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 181:

ACTAACCAG CATCGTTCGC AGGAAAATAA GGACAATAAT CGTGCTCTCTT ATGTGGATGG	60
CAGCCAGTCA AGTCAGAAAA GTGAAACTTT GACACCAGAC CAGGTTAGCC AGAAAGAAGG	120
AATTCAGGCT GAGCAAATTG TAATCAAAAT TACAGATCAG GGCTATGTAA CGTCACACGG	180
TGACCACTAT CATTACTATA ATGGGAAAGT TCCTTATGAT GCCCTCTTTA GTGAAGAACT	240
CTTGATGAAG GATCCAACT ATCAACTTAA AGACGCTGAT ATTGTCAATG AAGTCAAGGG	300
TGGTTATATC ATCAAGGTCG ATGGAAAATA TTATGTCTAC CTGAAAGATG CAGCTCATGC	360
TGATAATGTT CGAACTAAAG ATGAAATCAA TCGTCAAAAA CAAGAACATG TCAAAGATAA	420
TGAGAAGGTT AACTCTAATG TTGCTGTAGC AAGGTCTCAG GGACGATATA CGACAAATGA	480
TGGTTATGTC TTTAATCCAG CTGATATTAT CGAAGATACG GGTAATGCTT ATATCGTTCC	540
TCATGGAGGT CACTATCACT ACATTCCCAA AAGCGATTTA TCTGCTAGTG AATTAGCAGC	600
AGCTAAAGCA CATCTGGCTG GAAAAAATAT GCAACCGAGT CAGTTAAGCT ATTCTTCAAC	660
AGCTAGTGAC AATAACACGC AATCTGTAGC AAAAGGATCA ACTAGCAAGC CAGCAAATAA	720
ATCTGAAAAT CTCCAGAGTC TTTTGAAGGA ACTCTATGAT TCACCTAGCG CCCAACGTTA	780
CAGTGAATCA GATGGCCTGG TCTTTGACCC TGCTAAGATT ATCAGTCGTA CACCAAATGG	840
AGTTGCGATT CCGCATGGCG ACCATTACCA CTTTATTCCT TACAGCAAGC TTTCTGCCTT	900
AGAAGAAAAG ATTGCCAGAA TGGTGCCTAT CAGTGGAAGT GGTCTACAG TTTCTACAAA	960
TGCAAAACCT AATGAAGTAG TGTCTAGTCT AGGCAGTCTT TCAAGCAATC CTTCTTCTTT	1020
AACGACAAGT AAGGAGCTCT CTTCAGCATC TGATGGTTAT ATTTTAAATC CAAAAGATAT	1080
CGTTGAAGAA ACGGCTACAG CTTATATTGT AAGACATGGT GATCATTTCC ATTACATTCC	1140
AAAATCAAAT CAAATTGGGC AACCGACTCT TCCAAACAAT AGTCTAGCAA CACCTTCTCC	1200

ATCTCTTCCA ATCAATCCAG GAACTTCACA TGAGAAACAT GAAGAAGATG GATACGGATT 1260
 TGATGCTAAT CGTATTATCG CTGAAGATGA ATCAGGTTTT GTCATGAGTC ACGGAGACCA 1320
 CAATCATTAT TTCTTCAAGA AG 1342

(2) INFORMATION FOR SEQ ID NO:182:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 447 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:182:

Leu Asn Gln His Arg Ser Gln Glu Asn Lys Asp Asn Asn Arg Val Ser
 1 5 10 15
 Tyr Val Asp Gly Ser Gln Ser Ser Gln Lys Ser Glu Asn Leu Thr Pro
 20 25 30
 Asp Gln Val Ser Gln Lys Glu Gly Ile Gln Ala Glu Gln Ile Val Ile
 35 40 45
 Lys Ile Thr Asp Gln Gly Tyr Val Thr Ser His Gly Asp His Tyr His
 50 55 60
 Tyr Tyr Asn Gly Lys Val Pro Tyr Asp Ala Leu Phe Ser Glu Glu Leu
 65 70 75 80
 Leu Met Lys Asp Pro Asn Tyr Gln Leu Lys Asp Ala Asp Ile Val Asn
 85 90 95
 Glu Val Lys Gly Gly Tyr Ile Ile Lys Val Asp Gly Lys Tyr Tyr Val
 100 105 110
 Tyr Leu Lys Asp Ala Ala His Ala Asp Asn Val Arg Thr Lys Asp Glu
 115 120 125
 Ile Asn Arg Gln Lys Gln Glu His Val Lys Asp Asn Glu Lys Val Asn
 130 135 140
 Ser Asn Val Ala Val Ala Arg Ser Gln Gly Arg Tyr Thr Thr Asn Asp
 145 150 155 160
 Gly Tyr Val Phe Asn Pro Ala Asp Ile Ile Glu Asp Thr Gly Asn Ala
 165 170 175
 Tyr Ile Val Pro His Gly Gly His Tyr His Tyr Ile Pro Lys Ser Asp
 180 185 190
 Leu Ser Ala Ser Glu Leu Ala Ala Ala Lys Ala His Leu Ala Gly Lys
 195 200 205
 Asn Met Gln Pro Ser Gln Leu Ser Tyr Ser Ser Thr Ala Ser Asp Asn
 210 215 220
 Asn Thr Gln Ser Val Ala Lys Gly Ser Thr Ser Lys Pro Ala Asn Lys

225		230		235		240									
Ser	Glu	Asn	Leu	Gln	Ser	Leu	Leu	Lys	Glu	Leu	Tyr	Asp	Ser	Pro	Ser
				245					250					255	
Ala	Gln	Arg	Tyr	Ser	Glu	Ser	Asp	Gly	Leu	Val	Phe	Asp	Pro	Ala	Lys
			260					265					270		
Ile	Ile	Ser	Arg	Thr	Pro	Asn	Gly	Val	Ala	Ile	Pro	His	Gly	Asp	His
		275					280					285			
Tyr	His	Phe	Ile	Pro	Tyr	Ser	Lys	Leu	Ser	Ala	Leu	Glu	Glu	Lys	Ile
	290					295					300				
Ala	Arg	Met	Val	Pro	Ile	Ser	Gly	Thr	Gly	Ser	Thr	Val	Ser	Thr	Asn
305					310					315					320
Ala	Lys	Pro	Asn	Glu	Val	Val	Ser	Ser	Leu	Gly	Ser	Leu	Ser	Ser	Asn
			325						330					335	
Pro	Ser	Ser	Leu	Thr	Thr	Ser	Lys	Glu	Leu	Ser	Ser	Ala	Ser	Asp	Gly
			340					345					350		
Tyr	Ile	Phe	Asn	Pro	Lys	Asp	Ile	Val	Glu	Glu	Thr	Ala	Thr	Ala	Tyr
		355					360					365			
Ile	Val	Arg	His	Gly	Asp	His	Phe	His	Tyr	Ile	Pro	Lys	Ser	Asn	Gln
	370					375					380				
Ile	Gly	Gln	Pro	Thr	Leu	Pro	Asn	Asn	Ser	Leu	Ala	Thr	Pro	Ser	Pro
385					390					395					400
Ser	Leu	Pro	Ile	Asn	Pro	Gly	Thr	Ser	His	Glu	Lys	His	Glu	Glu	Asp
			405						410					415	
Gly	Tyr	Gly	Phe	Asp	Ala	Asn	Arg	Ile	Ile	Ala	Glu	Asp	Glu	Ser	Gly
			420					425					430		
Phe	Val	Met	Ser	His	Gly	Asp	His	Asn	His	Tyr	Phe	Phe	Lys	Lys	
		435					440					445			

(2) INFORMATION FOR SEQ ID NO: 183:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 934 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 183:

TGACTACCTT GAAATCCCAC TTTACAGCTA TCTTGGTGGA TTCAACACTA AAGTTCTTCC	60
AACTCCAATG ATGAACATCA TCAACGGTGG TTCTCACTCT GACGCTCCAA TCGCTTTCCA	120
AGAGTTCATG ATCTTGCCAG TTGGTGC GCC AACATTTAAA GAAGCCCTTC GTTACGGTGC	180
TGAAATCTTC CACGCTCTTA AGAAAATCCT TAAATCACGT GGT TTGGAAA CTGCCGTAGG	240
TGACGAAGGT GGATTCGCTC CTCGTTTCGA AGGAACTGAA GATGGTGTTG AACTATCCT	300

145		150		155		160
Lys Tyr Pro Ile Ile Thr Ile Glu Asp Gly Met Asp Glu Asn Asp Trp						
	165			170		175
Asp Gly Trp Lys Ala Leu Thr Glu Arg Leu Gly Lys Lys Val Gln Leu						
	180			185		190
Val Gly Asp Asp Phe Phe Val Thr Asn Thr Asp Tyr Leu Ala Arg Gly						
	195		200			205
Ile Gln Glu Gly Ala Ala Asn Ser Ile Leu Ile Lys Val Asn Gln Ile						
	210		215			220
Gly Thr Leu Thr Glu Thr Phe Glu Ala Ile Glu Met Ala Lys Glu Ala						
	225		230		235	240
Gly Tyr Thr Ala Val Val Ser His Arg Ser Gly Glu Thr Glu Asp Ser						
	245			250		255
Thr Ile Ala Asp Ile Ala Val Ala Thr Asn Ala Gly Gln Ile Lys Thr						
	260			265		270
Gly Ser Leu Ser Arg Thr Asp Arg Ile Ala Lys Tyr Asn Gln Leu Leu						
	275		280			285
Arg Ile Glu Asp Gln Leu Gly Glu Val Ala Glu Tyr Arg Gly Leu Lys						
	290		295			300
Ser Phe Tyr Asn Leu Lys Lys						
	305		310			

(2) INFORMATION FOR SEQ ID NO: 185:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 541 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 185:

TCGTATCTTT TTTTGGAGCA ATGTTGCGGT AGAAGGACAT TCCATGGATC CGACCCTAGC	60
GGATGGCGAA ATTCTCTTCG TTGTAAACA CCTTCCTATT GACCGTTTGT ATATCGTGGT	120
GGCCCATGAG GAAGATGGCA ATAAGGACAT CGTCAAGCGC GTGATTGGAA TGCCTGGCGA	180
CACCATTCGT TACGAAAATG ATAAACTCTA CATCAATGAC AAAGAAACGG ACGAGCCTTA	240
TCTAGCAGAC TATATCAAAC GCTTCAAGGA TGACAAACTC CAAAGCACTT ACTCAGGCAA	300
GGGCTTTGAA GGAAATAAAG GAACTTTCTT TAGAAGTATC GCTCAAAAAG CTCAAGCCTT	360
CACAGTTGAT GTCAACTACA ACACCAACTT TAGCTTTACT GTTCCAGAAG GAGAATACCT	420
TCTCCTCGGA GATGACCGCT TGGTTTCGAG CGACAGCCGC CACGTAGGTA CCTTCAAAGC	480
AAAAGATATC ACAGGGGAAG CTAAATTCCG CTTATGGCCA ATCACCCGTA TCGGAACATT	540

(2) INFORMATION FOR SEQ ID NO:186:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 180 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:186:

Arg Ile Phe Phe Trp Ser Asn Val Arg Val Glu Gly His Ser Met Asp
 1 5 10 15
 Pro Thr Leu Ala Asp Gly Glu Ile Leu Phe Val Val Lys His Leu Pro
 20 25 30
 Ile Asp Arg Phe Asp Ile Val Val Ala His Glu Glu Asp Gly Asn Lys
 35 40 45
 Asp Ile Val Lys Arg Val Ile Gly Met Pro Gly Asp Thr Ile Arg Tyr
 50 55 60
 Glu Asn Asp Lys Leu Tyr Ile Asn Asp Lys Glu Thr Asp Glu Pro Tyr
 65 70 75 80
 Leu Ala Asp Tyr Ile Lys Arg Phe Lys Asp Asp Lys Leu Gln Ser Thr
 85 90 95
 Tyr Ser Gly Lys Gly Phe Glu Gly Asn Lys Gly Thr Phe Phe Arg Ser
 100 105 110
 Ile Ala Gln Lys Ala Gln Ala Phe Thr Val Asp Val Asn Tyr Asn Thr
 115 120 125
 Asn Phe Ser Phe Thr Val Pro Glu Gly Glu Tyr Leu Leu Leu Gly Asp
 130 135 140
 Asp Arg Leu Val Ser Ser Asp Ser Arg His Val Gly Thr Phe Lys Ala
 145 150 155 160
 Lys Asp Ile Thr Gly Glu Ala Lys Phe Arg Leu Trp Pro Ile Thr Arg
 165 170 175
 Ile Gly Thr Phe
 180

(2) INFORMATION FOR SEQ ID NO: 187:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 187:

GGACTCTCTC AAAGATGTGA AAGCAAATGC TAGCGACAGC AAGCCTGCAC AGGACAAGAA

GGATGCAAAA CAAGGAACGG AAGATAGTAA GGATTCAGAT AAGATGACTG AAACAAACTC 120
 AGTTCCGGCA GGAGTGATTG TGGTCAGTCT ACTTGCCCTC CTAGGCGTGA TTGCCTTCTG 180
 GCTGATTTCG CGTAAGAAAG AGTCAGAAAT CCAGCAATTA AGCACGGAAT TGATCAAGGT 240
 TCTAGGACAG CTAGATGCAG AAAAAGCGGA TAAAAAAGTC CTTGCCAAAG CCCAAAACCT 300
 TCTCCAAGAA ACCCTTGATT TCGTGAAAGA AGAAAATGGC TCAGCAGAGA CAGAAACTAA 360
 ACTAGTAGAG GAGCTTAAAG CAATCCTTGA CAAACTCAAG 400

(2) INFORMATION FOR SEQ ID NO:188:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 133 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:188:

Asp Ser Leu Lys Asp Val Lys Ala Asn Ala Ser Asp Ser Lys Pro Ala
 1 5 10 15

Gln Asp Lys Lys Asp Ala Lys Gln Gly Thr Glu Asp Ser Lys Asp Ser
 20 25 30

Asp Lys Met Thr Glu Thr Asn Ser Val Pro Ala Gly Val Ile Val Val
 35 40 45

Ser Leu Leu Ala Leu Leu Gly Val Ile Ala Phe Trp Leu Ile Arg Arg
 50 55 60

Lys Lys Glu Ser Glu Ile Gln Gln Leu Ser Thr Glu Leu Ile Lys Val
 65 70 75 80

Leu Gly Gln Leu Asp Ala Glu Lys Ala Asp Lys Lys Val Leu Ala Lys
 85 90 95

Ala Gln Asn Leu Leu Gln Glu Thr Leu Asp Phe Val Lys Glu Glu Asn
 100 105 110

Gly Ser Ala Glu Thr Glu Thr Lys Leu Val Glu Glu Leu Lys Ala Ile
 115 120 125

Leu Asp Lys Leu Lys
 130

(2) INFORMATION FOR SEQ ID NO: 189:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1201 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 189:

CAAGAAATCC TATCATCTCT TCCAGAAGCA AACAGAGACG AGGGGAATTC AGACTCAGTT 60
 GATTGAAGAA TCGCTTAGTC AGCAGACTAT AATCCAGTCC TTCAATGCTC AAACAGAATT 120
 TATCCAAAGA TTGCGTGAGG CTCATGACAA CTA CTCTCAGGC TATTCTCAGT CAGCCATCTT 180
 TTATTCTTCA ACGGTCAATC CTTGACTCG CTTTGTAAT GCACTCATTT ATGCCCTTTT 240
 AGCTGGAGTA GGAGCTTATC GTATCATGAT GGGTTCAGCC TTGACCGTCG GTCGTTTAGT 300
 GACTTTTTTTG AACTATGTTT AGCAATACAC CAAGCCCTTT AACGATATTT CTTCAGTGCT 360
 AGCTGAGTTG CAAAGTGCTC TGGCTTGCGT AGAGCGTATC TATGGAGTCT TAGATAGCCC 420
 TGAAGTGGCT GAAACAGGTA AGGAAGTCTT GACGACCAGT GACCAAGTTA AGGGAGCTAT 480
 TTCCTTTAAA CATGTCTCTT TTGGCTACCA TCCTGAAAAA ATTTTGATTA AGGACTTGTC 540
 TATCGATATT CCAGCTGGTA GTAAGGTAGC CATCGTTGGT CCGACAGGTG CTGGAAAATC 600
 AACTCTTATC AATCTCCTTA TGCCTTTTTT TCCATTAGC TCGGGAGATA TCTTGCTGGA 660
 TGGGCAATCC ATTTATGATT ATACACGAGT ATCATTGAGA CAGCAGTTTG GTATGGTGCT 720
 TCAAGAAACC TGGCTCACAC AAGGGACCAT TCATGATAAT ATTGCCTTTG GCAATCCTGA 780
 AGCCAGTCGA GAGCAAGTAA TTGCTGCTGC CAAAGCAGCT AATGCAGACT TTTTCATCCA 840
 ACAGTTGCCA CAGGGATACG ATACCAAGTT GGAAAATGCT GGAGAATCTC TCTCTGTCGG 900
 CCAAGCTCAG CTCTTGACCA TAGCCCGAGT CTTTCTGGCT ATTCCAAAGA TTCTTATCTT 960
 AGACGAGGCA ACTTCTTCCA TTGATACACG GACAGAAGTG CTGGTACAGG ATGCCTTTGC 1020
 AAAACTCATG AAGGGCCGCA CAAGTTTCAT CATTGCTCAC CGTTTGTCOA CCATTCAGGA 1080
 TGC GGATTTA ATTCTTGCT TAGTAGATGG TGATATTGTT GAATATGGTA ACCATCAAGA 1140
 ACTCATGGAT AGAAAGGGTA AGTATTACCA AATGCAAAAA GCTGCGGCTT TTAGTTCTGA 1200
 A 1201

(2) INFORMATION FOR SEQ ID NO:190:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:190:

Lys Lys Ser Tyr His Leu Phe Gln Lys Gln Thr Glu Thr Arg Gly Ile
 1 5 10 15
 Gln Thr Gln Leu Ile Glu Glu Ser Leu Ser Gln Gln Thr Ile Ile Gln
 20 25 30

Ser Phe Asn Ala Gln Thr Glu Phe Ile Gln Arg Leu Arg Glu Ala His
 35 40 45
 Asp Asn Tyr Ser Gly Tyr Ser Gln Ser Ala Ile Phe Tyr Ser Ser Thr
 50 55 60
 Val Asn Pro Ser Thr Arg Phe Val Asn Ala Leu Ile Tyr Ala Leu Leu
 65 70 75 80
 Ala Gly Val Gly Ala Tyr Arg Ile Met Met Gly Ser Ala Leu Thr Val
 85 90 95
 Gly Arg Leu Val Thr Phe Leu Asn Tyr Val Gln Gln Tyr Thr Lys Pro
 100 105 110
 Phe Asn Asp Ile Ser Ser Val Leu Ala Glu Leu Gln Ser Ala Leu Ala
 115 120 125
 Cys Val Glu Arg Ile Tyr Gly Val Leu Asp Ser Pro Glu Val Ala Glu
 130 135 140
 Thr Gly Lys Glu Val Leu Thr Thr Ser Asp Gln Val Lys Gly Ala Ile
 145 150 155 160
 Ser Phe Lys His Val Ser Phe Gly Tyr His Pro Glu Lys Ile Leu Ile
 165 170 175
 Lys Asp Leu Ser Ile Asp Ile Pro Ala Gly Ser Lys Val Ala Ile Val
 180 185 190
 Gly Pro Thr Gly Ala Gly Lys Ser Thr Leu Ile Asn Leu Leu Met Arg
 195 200 205
 Phe Tyr Pro Ile Ser Ser Gly Asp Ile Leu Leu Asp Gly Gln Ser Ile
 210 215 220
 Tyr Asp Tyr Thr Arg Val Ser Leu Arg Gln Gln Phe Gly Met Val Leu
 225 230 235 240
 Gln Glu Thr Trp Leu Thr Gln Gly Thr Ile His Asp Asn Ile Ala Phe
 245 250 255
 Gly Asn Pro Glu Ala Ser Arg Glu Gln Val Ile Ala Ala Ala Lys Ala
 260 265 270
 Ala Asn Ala Asp Phe Phe Ile Gln Gln Leu Pro Gln Gly Tyr Asp Thr
 275 280 285
 Lys Leu Glu Asn Ala Gly Glu Ser Leu Ser Val Gly Gln Ala Gln Leu
 290 295 300
 Leu Thr Ile Ala Arg Val Phe Leu Ala Ile Pro Lys Ile Leu Ile Leu
 305 310 315 320
 Asp Glu Ala Thr Ser Ser Ile Asp Thr Arg Thr Glu Val Leu Val Gln
 325 330 335
 Asp Ala Phe Ala Lys Leu Met Lys Gly Arg Thr Ser Phe Ile Ile Ala
 340 345 350
 His Arg Leu Ser Thr Ile Gln Asp Ala Asp Leu Ile Leu Val Leu Val
 355 360 365

Asp Gly Asp Ile Val Glu Tyr Gly Asn His Gln Glu Leu Met Asp Arg
 370 375 380

Lys Gly Lys Tyr Tyr Gln Met Gln Lys Ala Ala Ala Phe Ser Ser Glu
 385 390 395 400

(2) INFORMATION FOR SEQ ID NO: 191:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1033 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 191:

ACGAAATGCA GGGCAGACAG ATGCCTCGCA AATTGAAAAG GCGGCAGTTA GCCAAGGAGG	60
AAAAGCAGTG AAAAAACAG AAATTAGTAA AGACGCAGAC TTGCACGAAA TTTATCTAGC	120
TGGAGGTTGT TTCTGGGGAG TGGAGGAATA TTTCTCACGT GTTCCCGGGG TGACGGATGC	180
CGTTTCAGGC TATGCAAATG GTAGAGGAGA AACAAACCAAG TACGAATTGA TTAACCAAAC	240
AGGTCATGCA GAAACCGTCC ATGTCACCTA TGATGCCAAG CAAATTTCTC TCAAGGAAAT	300
CCTGCTTCAC TATTTCCGCA TTATCAATCC AACCAGCAA AATAACAAG GAAATGATGT	360
GGGGACCCAG TACCGTACTG GTGTTTATTA CACAGATGAC AAGGATTGG AAGTGATTAA	420
CCAAGTCTTT GATGAGGTGG CTAAGAAATA CGATCAACCT CTAGCAGTTG AAAAGGAAAA	480
CTTGAAGAAT TTTGTGGTGG CTGAGGATTA CCATCAAGAC TATCTCAAGA AAAATCCAA	540
TGGCTACTGC CATATCAATG TTAATCAGGC GGCCTATCCT GTCATTGATG CCAGCAAATA	600
TCCAAAACCA AGTGATGAGG AATTGAAAA GACCCTGTCA CCTGAGGAGT ATGCAGTTAC	660
CCAGGAAAT CAAACAGAAC GAGCTTTCTC AAACCGTTAC TGGGATAAAT TTGAATCCGG	720
TATCTATGTG GATATAGCAA CTGGGGAACC TCTCTTTTCA TCAAAGACA AATTGAGTC	780
TGGTTGTGGC TGGCCTAGTT TTACCCAACC CATCAGTCCA GATGTTGTCA CCTACAAGGA	840
AGATAAGTCC TACAATATGA CGCGTATGGA AGTGCGGAGC CGAGTAGGAG ATTCTCACCT	900
TGGGCATGTC TTTACGGATG GTCCACAGGA CAAGGGCGGC TTACGTTACT GTATCAATAG	960
CCTCTCTATC CGCTTTATTC CCAAAGACCA AATGGAAGAA AAAGGCTACG CTTATTTACT	1020
AGATTATGTT GAT	1033

(2) INFORMATION FOR SEQ ID NO:192:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 344 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

Ala Tyr Leu Leu Asp Tyr Val Asp
340

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 396 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

TGTATAGTTT	TTAGCGCTTG	TTCTTCTAAT	TCTGNTAAAA	ATGAAGAAAA	TACTTCTAAA	60
GAGCATGCGC	CTGATAAAAT	AGTTTTAGAT	CATGCTTTCG	GTCAAACAT	ATTAGATAAA	120
AAACCTGAAA	GAGTTGCAAC	TATTGCTTGG	GGAAATCATG	ATGTAGCATT	AGCTTTAGGA	180
ATAGTTCCTG	TTGGATTTTC	AAAAGCAAAT	TACGGTGTA	GTGCTGATA	AGGAGTTTTA	240
CCATGGACAG	AAGAAAAAAT	CAAAGAACTA	AATGGTAAAG	CTAACCTATT	TGACGATTTG	300
GATGGACTTA	ACTTTGAAGC	AATATCAAAT	TCTAAACCAG	ATGTTATCTT	AGCAGGTTAT	360
TCTGGTATAA	CTAAAGAAGA	TTATGACACT	CTATCA			396

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 132 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:194:

Pro. Trp Thr Glu Glu Lys Ile Lys Glu Leu Asn Gly Lys Ala Asn Leu
85 90 95

Asp Thr Leu Ser
130

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 844 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

GTGTGTCGAG	CATATTCTGA	AGCAAACCTA	TCAAAATATA	GAAATTATTT	TAGTTGATGA	60
CGGTTCTACG	GATAATTCTG	GGGAAATTTG	TGATGCTTTT	ATGATGCAAG	ATAATCGTGT	120
GCGAGTATTG	CATCAAGAAA	ATAAGGGGGG	GGCAGCACAA	GCTAAAAATA	TGGGGATTAG	180
TGTAGCTAAG	GGAGAGTACA	TCACGATTGT	TGATTTCAGAT	GATATCGTAA	AAGAAAATAT	240
GATTGAAACT	CTTTATCAGC	AAGTCCAAGA	AAAGGATGCA	GATGTTGTTA	TAGGGAATTA	300
CTATAATTAT	GACGAAAGTG	ACGGGAATTT	TTATTTTAT	GTAACAGGGC	AAGATTTTTG	360
CGTCGAAGAA	TTAGCTATAC	AAGAAATTAT	GAACCGTCAA	GCAGGAGATT	GGAAATTCAA	420
TAGCTCGGCC	TTTATATTGC	CGACATTTAA	GTTGATTAAA	AAAGAATTAT	TCAATGAAGT	480
TCACTTTTCA	AATGGTCGCC	GCTTTGATGA	TGAAGCAACT	ATGCATCGCT	TTTATCTTTT	540
AGCCTCTAAA	ATCGTCTTTA	TAAACGATAA	TCTCTATCTG	TATAGAAGAC	GTTCAGGAAG	600
CATCATGAGA	ACGGAATTTG	ATCTTTCCTG	GGCAAGAGAT	ATTGTTGAAG	TGTTTTCTAA	660
GAAATATATCG	GATTGTGTCT	TGGCTGGTTT	GGATGTCTCC	GTTCTGCGTA	TTCGATTTGT	720
CAATCTTTTA	AAAGATTATA	AGCAAACTTT	AGAATACCAT	CAATTAACAG	ATACTGAGGA	780
ATATAAAGAT	ATTTGTTTCA	GATTAAAGTT	GTTTTTTGAT	GCAGAACAAA	GAAATGGTAA	840
AAGT						844

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 281 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:196:

Cys Val Glu His Ile Leu Lys Gln Thr Tyr Gln Asn Ile Glu Ile Ile
 1 5 10 15
 Leu Val Asp Asp Gly Ser Thr Asp Asn Ser Gly Glu Ile Cys Asp Ala
 20 25 30
 Phe Met Met Gln Asp Asn Arg Val Arg Val Leu His Gln Glu Asn Lys
 35 40 45
 Gly Gly Ala Ala Gln Ala Lys Asn Met Gly Ile Ser Val Ala Lys Gly
 50 55 60
 Glu Tyr Ile Thr Ile Val Asp Ser Asp Asp Ile Val Lys Glu Asn Met
 65 70 75 80
 Ile Glu Thr Leu Tyr Gln Gln Val Gln Glu Lys Asp Ala Asp Val Val
 85 90 95
 Ile Gly Asn Tyr Tyr Asn Tyr Asp Glu Ser Asp Gly Asn Phe Tyr Phe
 100 105 110
 Tyr Val Thr Gly Gln Asp Phe Cys Val Glu Glu Leu Ala Ile Gln Glu
 115 120 125
 Ile Met Asn Arg Gln Ala Gly Asp Trp Lys Phe Asn Ser Ser Ala Phe
 130 135 140
 Ile Leu Pro Thr Phe Lys Leu Ile Lys Lys Glu Leu Phe Asn Glu Val
 145 150 155 160
 His Phe Ser Asn Gly Arg Arg Phe Asp Asp Glu Ala Thr Met His Arg
 165 170 175
 Phe Tyr Leu Leu Ala Ser Lys Ile Val Phe Ile Asn Asp Asn Leu Tyr
 180 185 190
 Leu Tyr Arg Arg Arg Ser Gly Ser Ile Met Arg Thr Glu Phe Asp Leu
 195 200 205
 Ser Trp Ala Arg Asp Ile Val Glu Val Phe Ser Lys Lys Ile Ser Asp
 210 215 220
 Cys Val Leu Ala Gly Leu Asp Val Ser Val Leu Arg Ile Arg Phe Val
 225 230 235 240
 Asn Leu Leu Lys Asp Tyr Lys Gln Thr Leu Glu Tyr His Gln Leu Thr
 245 250 255
 Asp Thr Glu Glu Tyr Lys Asp Ile Cys Phe Arg Leu Lys Leu Phe Phe
 260 265 270
 Asp Ala Glu Gln Arg Asn Gly Lys Ser
 275 280

(2) INFORMATION FOR SEQ ID NO: 197:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 811 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

F00001.013001

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 197:

GTGTTTGGAT AGCATTGAGA ATCAGACGTA TCAAAATTTT GAGTGTAT TAATCAATGA 60
 TGGCTCTCCA GATCATTGAT CCAAAATATG TGAAGAATTT GTAGAGAAAG ATTCTCGTTT 120
 CAAATATTTT GAGAAAGCAA ACGGCGGTCT TTCATCAGCT CGTAACCTAG GTATTGAATG 180
 TTCGGGGGGG GCGTACATTA CTTTTGTAGA CTCTGATGAT TGGTTGGAAC ATGATGCTTT 240
 AGACCGATTA TATGGTGCTT TGAAAAAGGA AAACGCAGAT ATTAGTATCG GCGTTATAA 300
 TTCTTATGAT GAAACACGCT ATGTGTATAT GACTTATGTT ACGGATCCAG ATGATTCTCT 360
 AGAAGTGATA GAAGGTAAAG CAATTATGGA TAGGGAAGGT GTCGAAGAAG TCAGAAATGG 420
 GAACTGGACT GTAGCTGTCT TGAAGTTATT CAAGAGAGAG TTACTACAAG ATTTACCATT 480
 TCCTATAGGA AAAATTGCAG AGGATACTTA CTGGACATGG AAGGTACTTC TAAGAGCTTC 540
 GAGGATAGTC TATTTGAATC GTTGTGTTTA CTGGTACCGT GTTGGTTTAT CTGATACTTT 600
 ATCGAATACA TGGAGTGAAA AGCGTATGTA TGATGAAATT GGGGCTAGGG AAGAAAAGAT 660
 AGCTATTTTA GCAAGTTCAG ACTATGACTT GACCAATCAT ATTTTGATTT ATAAAAATAG 720
 ATTACAAAGA GTGATAGCAA AATTAGAAGA ACAAATATG CAGTTCACAG AGATTACAG 780
 AAGAATGATG GAAAAATTGT CTTTACTTCC G 811

(2) INFORMATION FOR SEQ ID NO:198:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 270 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:198:

Cys Leu Asp Ser Ile Gln Asn Gln Thr Tyr Gln Asn Phe Glu Cys Leu
 1 5 10 15
 Leu Ile Asn Asp Gly Ser Pro Asp His Ser Ser Lys Ile Cys Glu Glu
 20 25 30
 Phe Val Glu Lys Asp Ser Arg Phe Lys Tyr Phe Glu Lys Ala Asn Gly
 35 40 45
 Gly Leu Ser Ser Ala Arg Asn Leu Gly Ile Glu Cys Ser Gly Gly Ala
 50 55 60
 Tyr Ile Thr Phe Val Asp Ser Asp Asp Trp Leu Glu His Asp Ala Leu
 65 70 75 80
 Asp Arg Leu Tyr Gly Ala Leu Lys Lys Glu Asn Ala Asp Ile Ser Ile
 85 90 95

300.

Gly Arg Tyr Asn Ser Tyr Asp Glu Thr Arg Tyr Val Tyr Met Thr Tyr
100 105 110

Val Thr Asp Pro Asp Asp Ser Leu Glu Val Ile Glu Gly Lys Ala Ile
115 120 125

Met Asp Arg Glu Gly Val Glu Glu Val Arg Asn Gly Asn Trp Thr Val
130 135 140

Ala Val Leu Lys Leu Phe Lys Arg Glu Leu Leu Gln Asp Leu Pro Phe
145 150 155 160

Pro Ile Gly Lys Ile Ala Glu Asp Thr Tyr Trp Thr Trp Lys Val Leu
165 170 175

Leu Arg Ala Ser Arg Ile Val Tyr Leu Asn Arg Cys Val Tyr Trp Tyr
180 185 190

Arg Val Gly Leu Ser Asp Thr Leu Ser Asn Thr Trp Ser Glu Lys Arg
195 200 205

Met Tyr Asp Glu Ile Gly Ala Arg Glu Glu Lys Ile Ala Ile Leu Ala
210 215 220

Ser Ser Asp Tyr Asp Leu Thr Asn His Ile Leu Ile Tyr Lys Asn Arg
225 230 235 240

Leu Gln Arg Val Ile Ala Lys Leu Glu Glu Gln Asn Met Gln Phe Thr
245 250 255

Glu Ile Tyr Arg Arg Met Met Glu Lys Leu Ser Leu Leu Pro
260 265 270

(2). INFORMATION FOR SEQ ID NO: 199:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2023 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 199:

GTGCCTAGAT AGTATTATTA CTCAACATA TAAAAATATT GAGATTGTTG TCGTTAATGA	60
TGGTTCTACG GATGCTTCAG GTGAAATTTG TAAAGAATTT TCAGAAATGG ATCACCGAAT	120
TCTCTATATA GAACAAGAAA ATGCTGGTCT TTCTGCCGCA CGAAACACCG GTCTGAATAA	180
TATGTCCGGA AATTATGTGA CCTTTGTGGA CTCGGATGAT TGGATTGAGC AAGATTATGT	240
AGAAACTCTA TATAAAAAA TAGTAGAGTA TCAGGCTGAT ATTGCAGTTG GTAATTATTA	300
TTCTTTCAAC GAAAGTGAAG GAATGTTCTA CTTTCATATA TTGGGAGACT CCTATTATGA	360
GAAAGTATAT GATAATGTTT CTATCTTTGA GAACTTGTAT GAAACTCAAG AAATGAAGAG	420
TTTTGCTTTG ATATCTGCTT GGGGTAAACT CTATAAGGCA AGATTGTTTG AGCAGTTGCG	480
CTTTGACATA GGTAAATTAG GAGAAGATGG TTACCTCAAT CAAAAGGTAT ATTTATTATC	540

AGAAAAGGTA ATTTATTTAA ATAAAAGTCT TTATGCTTAT CGGATTAGAA AAGGTAGTTT 600
 ATCAAGAGTT TGGACAGAAA AGTGGATGCA CGCTTTAGTT GATGCTATGT CTGAACGTAT 660
 TACGCTACTA GCTAATATGG GTTATCCTCT AGAGAAACAC TTGGCAGTTT ATCGTCAGAT 720
 GTTGGAAGTC AGTCTCGCCA ACGGTCAAGC TAGTGGTTTA TCTGACACAG CAACGTATAA 780
 AGAGTTTGAA ATGAAACAAA GGCTTTTAAA TCAGCTATCG AGACAAGAGG AAAGTGAAAA 840
 GAAAGCCATT GTCCTCGCAG CAACTATGG CTATGTAGAC CAAGTTTTAA CGACAATCAA 900
 GTCTATTTGT TATCATAATC GTTCGATTCG TTTTATCTG ATTCATAGCG ATTTTCCAAA 960
 TGAATGGATT AAGCAATTAA ATAAGCGCTT AGAGAAGTTT GACTCAGAAA TTATTAATTG 1020
 TCGGGTAACT TCTGAGCAAA TTTCATGTTA TAAATCGGAT ATTAGTTACA CAGTCTTTTT 1080
 ACGCTATTTT ATAGCTGATT TCGTGCAAGA AGACAAGGCC CTCTACTTGG ACTGTGATCT 1140
 AGTTGTAACG AAAAATCTGG ATGACTTGTT TGCTACAGAC TTACAAGATT ATCCTTTGGC 1200
 TGCTGTTAGA GATTTTGGGG GCAGAGCTTA TTTTGGTCAA GAAATCTTTA ATGCCGGTGT 1260
 TCTCTTGGTA AACAATGCTT TTTGGAAAAA AGAGAATATG ACCCAAAAAT TAATTGATGT 1320
 AACCAATGAA TGGCATGATA AGGTGGATCA GGCAGATCAG AGCATCTTGA ATATGCTTTT 1380
 TGAACATAAA TGGTTGGAAT TGGACTTTGA TTATAATCAT ATTGTCATTC ATAAACAGTT 1440
 TGCTGATTAT CAATTGCCTG AGGGTCAGGA TTATCCTGCT ATTATTCATC ATCTTTCTCA 1500
 TCGGAAACCG TGGAAAGATT TGGCGGCCCA AACCTATCGT GAAGTTTGGT GGTACTATCA 1560
 TGGGCTTGAA TGGACAGAAT TGGGACAAAA CCATCATTTA CATCCATTAC AAAGATCTCA 1620
 CATCTATCCA ATAAAGGAAC CTTTCACTTG TCTAATCTAT ACTGCCTCAG ACCATATTGA 1680
 ACAAATTGAG ACATTGGTTC AATCCTTGCC TGATATTCAG TTTAAGATAG CAGCTAGAGT 1740
 AATAGTTAGT GATCGATTGG CTCAGATGAC AATTTATCCA AACGTGACTA TATTTAACGG 1800
 AATTCATCTAT TTGGTAGATG TCGATAATGA ATTGGTAGAA ACCAGTCAAG TACTTTTAGA 1860
 TATTAATCAT GCGGAAAAGA CAGAAGAAAT TCTCGATCAA TTTGCTAATC TTGGCAAGCC 1920
 TATCTTATCC TTTGAAAATA CTAAACCTA TGAAGTAGGT CAGGAGGCAT ATGCTGTTGA 1980
 CCAAGTTCAA GCAATGATTG AAAAATTGAG AGAAATAAGC AAA 2023

(2) INFORMATION FOR SEQ ID NO:200:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 674 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

____(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:200:

Cys Leu Asp Ser Ile Ile Thr Gln Thr Tyr Lys Asn Ile Glu Ile Val
 1 5 10 15
 Val Val Asn Asp Gly Ser Thr Asp Ala Ser Gly Glu Ile Cys Lys Glu
 20 25 30
 Phe Ser Glu Met Asp His Arg Ile Leu Tyr Ile Glu Gln Glu Asn Ala
 35 40 45
 Gly Leu Ser Ala Ala Arg Asn Thr Gly Leu Asn Asn Met Ser Gly Asn
 50 55 60
 Tyr Val Thr Phe Val Asp Ser Asp Asp Trp Ile Glu Gln Asp Tyr Val
 65 70 75 80
 Glu Thr Leu Tyr Lys Lys Ile Val Glu Tyr Gln Ala Asp Ile Ala Val
 85 90 95
 Gly Asn Tyr Tyr Ser Phe Asn Glu Ser Glu Gly Met Phe Tyr Phe His
 100 105 110
 Ile Leu Gly Asp Ser Tyr Tyr Glu Lys Val Tyr Asp Asn Val Ser Ile
 115 120 125
 Phe Glu Asn Leu Tyr Glu Thr Gln Glu Met Lys Ser Phe Ala Leu Ile
 130 135 140
 Ser Ala Trp Gly Lys Leu Tyr Lys Ala Arg Leu Phe Glu Gln Leu Arg
 145 150 155 160
 Phe Asp Ile Gly Lys Leu Gly Glu Asp Gly Tyr Leu Asn Gln Lys Val
 165 170 175
 Tyr Leu Leu Ser Glu Lys Val Ile Tyr Leu Asn Lys Ser Leu Tyr Ala
 180 185 190
 Tyr Arg Ile Arg Lys Gly Ser Leu Ser Arg Val Trp Thr Glu Lys Trp
 195 200 205
 Met His Ala Leu Val Asp Ala Met Ser Glu Arg Ile Thr Leu Leu Ala
 210 215 220
 Asn Met Gly Tyr Pro Leu Glu Lys His Leu Ala Val Tyr Arg Gln Met
 225 230 235 240
 Leu Glu Val Ser Leu Ala Asn Gly Gln Ala Ser Gly Leu Ser Asp Thr
 245 250 255
 Ala Thr Tyr Lys Glu Phe Glu Met Lys Gln Arg Leu Leu Asn Gln Leu
 260 265 270
 Ser Arg Gln Glu Glu Ser Glu Lys Lys Ala Ile Val Leu Ala Ala Asn
 275 280 285
 Tyr Gly Tyr Val Asp Gln Val Leu Thr Thr Ile Lys Ser Ile Cys Tyr
 290 295 300
 His Asn Arg Ser Ile Arg Phe Tyr Leu Ile His Ser Asp Phe Pro Asn
 305 310 315 320
 Glu Trp Ile Lys Gln Leu Asn Lys Arg Leu Glu Lys Phe Asp Ser Glu
 325 330 335

00765374 042004
 100207 1259260

Ile	Ile	Asn	Cys	Arg	Val	Thr	Ser	Glu	Ile	Ser	Cys	Tyr	Lys	Ser	
														340	
														345	
														350	
Asp	Ile	Ser	Tyr	Thr	Val	Phe	Leu	Arg	Tyr	Phe	Ile	Ala	Asp	Phe	Val
														355	
Gln	Glu	Asp	Lys	Ala	Leu	Tyr	Leu	Asp	Cys	Asp	Leu	Val	Val	Thr	Lys
														370	
Asn	Leu	Asp	Asp	Leu	Phe	Ala	Thr	Asp	Leu	Gln	Asp	Tyr	Pro	Leu	Ala
														385	
Ala	Val	Arg	Asp	Phe	Gly	Gly	Arg	Ala	Tyr	Phe	Gly	Gln	Glu	Ile	Phe
														405	
Asn	Ala	Gly	Val	Leu	Leu	Val	Asn	Asn	Ala	Phe	Trp	Lys	Lys	Glu	Asn
														420	
Met	Thr	Gln	Lys	Leu	Ile	Asp	Val	Thr	Asn	Glu	Trp	His	Asp	Lys	Val
														435	
Asp	Gln	Ala	Asp	Gln	Ser	Ile	Leu	Asn	Met	Leu	Phe	Glu	His	Lys	Trp
														450	
Leu	Glu	Leu	Asp	Phe	Asp	Tyr	Asn	His	Ile	Val	Ile	His	Lys	Gln	Phe
														465	
Ala	Asp	Tyr	Gln	Leu	Pro	Glu	Gly	Gln	Asp	Tyr	Pro	Ala	Ile	Ile	His
														485	
Tyr	Leu	Ser	His	Arg	Lys	Pro	Trp	Lys	Asp	Leu	Ala	Ala	Gln	Thr	Tyr
														500	
Arg	Glu	Val	Trp	Trp	Tyr	Tyr	His	Gly	Leu	Glu	Trp	Thr	Glu	Leu	Gly
														515	
Gln	Asn	His	His	Leu	His	Pro	Leu	Gln	Arg	Ser	His	Ile	Tyr	Pro	Ile
														530	
Lys	Glu	Pro	Phe	Thr	Cys	Leu	Ile	Tyr	Thr	Ala	Ser	Asp	His	Ile	Glu
														545	
Gln	Ile	Glu	Thr	Leu	Val	Gln	Ser	Leu	Pro	Asp	Ile	Gln	Phe	Lys	Ile
														565	
Ala	Ala	Arg	Val	Ile	Val	Ser	Asp	Arg	Leu	Ala	Gln	Met	Thr	Ile	Tyr
														580	
Pro	Asn	Val	Thr	Ile	Phe	Asn	Gly	Ile	His	Tyr	Leu	Val	Asp	Val	Asp
														595	
Asn	Glu	Leu	Val	Glu	Thr	Ser	Gln	Val	Leu	Leu	Asp	Ile	Asn	His	Gly
														610	
Glu	Lys	Thr	Glu	Glu	Ile	Leu	Asp	Gln	Phe	Ala	Asn	Leu	Gly	Lys	Pro
														625	
Ile	Leu	Ser	Phe	Glu	Asn	Thr	Lys	Thr	Tyr	Glu	Val	Gly	Gln	Glu	Ala
														645	
Tyr	Ala	Val	Asp	Gln	Val	Gln	Ala	Met	Ile	Glu	Lys	Leu	Arg	Glu	Ile
														660	

Ser Lys

(2) INFORMATION FOR SEQ ID NO: 201:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 910 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 201:

CATTGAGAAG CAGACCTATC AAAATCTGGA AATTATTCTT GTTGATGATG GTGCAACAGA 60
 TGAAAGTGGT CGCTTGTTGTG ATTCAATCGC TGAACAAGAT GACAGGGTGT CAGTGCTTCA 120
 TAAAAAGAAC GAAGGATTGT CGCAAGCAGC AAATGATGGG ATGAAGCAGG CTCACGGGGA 180
 TTATCTGATT TTTATTGACT CAGATGATTA TATCCATCCA GAAATGATTC AGAGCTTATA 240
 TGAGCAATTA GTTCAAGAAG ATGCGGATGT TTCGAGCTGT GGTGTCATGA ATGTCTATGC 300
 TAATGATGAA AGCCACAGT CAGCCAATCA GGATGACTAT TTTGTCTGTG ATTCTCAAAC 360
 ATTTCTAAAG GAATACCTCA TAGGTGAAAA AATACCTGGG ACGATTTGCA ATAAGCTAAT 420
 CAAGAGACAG ATTGCAACTG CCCTATCCTT TCCTAAGGGG TTGATTTACG AAGATGCCTA 480
 TTACCATTTT GATTTAATCA AGTTGGCCAA GAAGTATGTG GTTAATACTA AACCCATTATTA 540
 TTACTATTTT CATAGAGGGG ATAGTATTAC GACCAAACCC TATGCAGAGA AGGATTTAGC 600
 CTATATTGAT ATCTACCAA AGTTTTATAA TGAAGTTGTG AAAAATATC CTGACTTGAA 660
 AGAGGTCGCT TTTTTCAGAT TGGCCTATGC CCACTTCTTT ATTCTGGATA AGATGTTGCT 720
 AGATGATCAG TATAACAGT TTGAAGCCTA TTCTCAGATT CATCGTTTTT TAAAAGGCCA 780
 TGCCTTTGCT ATTTCTAGGA ATCCAATTTT CCGTAAGGGG AGAAGAATTA GTGCTTTGGC 840
 CCTATTCATA AATATTCCT TATATCGATT CTTATTACTG AAAAATATTG AAAAATCTAA 900
 AAAATTACAT 910

(2) INFORMATION FOR SEQ ID NO:202:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 303 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:202:

Ile Gln Lys Gln Thr Tyr Gln Asn Leu Glu Ile Ile Leu Val Asp Asp
 1 5 10 15

Gly Ala Thr Asp Glu Ser Gly Arg Leu Cys Asp Ser Ile Ala Glu Gln
 20 25 30
 Asp Asp Arg Val Ser Val Leu His Lys Lys Asn Glu Gly Leu Ser Gln
 35 40 45
 Ala Arg Asn Asp Gly Met Lys Gln Ala His Gly Asp Tyr Leu Ile Phe
 50 55 60
 Ile Asp Ser Asp Asp Tyr Ile His Pro Glu Met Ile Gln Ser Leu Tyr
 65 70 75 80
 Glu Gln Leu Val Gln Glu Asp Ala Asp Val Ser Ser Cys Gly Val Met
 85 90 95
 Asn Val Tyr Ala Asn Asp Glu Ser Pro Gln Ser Ala Asn Gln Asp Asp
 100 105 110
 Tyr Phe Val Cys Asp Ser Gln Thr Phe Leu Lys Glu Tyr Leu Ile Gly
 115 120 125
 Glu Lys Ile Pro Gly Thr Ile Cys Asn Lys Leu Ile Lys Arg Gln Ile
 130 135 140
 Ala Thr Ala Leu Ser Phe Pro Lys Gly Leu Ile Tyr Glu Asp Ala Tyr
 145 150 155 160
 Tyr His Phe Asp Leu Ile Lys Leu Ala Lys Lys Tyr Val Val Asn Thr
 165 170 175
 Lys Pro Tyr Tyr Tyr Tyr Phe His Arg Gly Asp Ser Ile Thr Thr Lys
 180 185 190
 Pro Tyr Ala Glu Lys Asp Leu Ala Tyr Ile Asp Ile Tyr Gln Lys Phe
 195 200 205
 Tyr Asn Glu Val Val Lys Asn Tyr Pro Asp Leu Lys Glu Val Ala Phe
 210 215 220
 Phe Arg Leu Ala Tyr Ala His Phe Phe Ile Leu Asp Lys Met Leu Leu
 225 230 235 240
 Asp Asp Gln Tyr Lys Gln Phe Glu Ala Tyr Ser Gln Ile His Arg Phe
 245 250 255
 Leu Lys Gly His Ala Phe Ala Ile Ser Arg Asn Pro Ile Phe Arg Lys
 260 265 270
 Gly Arg Arg Ile Ser Ala Leu Ala Leu Phe Ile Asn Ile Ser Leu Tyr
 275 280 285
 Arg Phe Leu Leu Leu Lys Asn Ile Glu Lys Ser Lys Lys Leu His
 290 295 300

(2) INFORMATION FOR SEQ ID NO: 203:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1972 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

TAAGGCTGAT	AATCGTGTTT	AAATGAGAAC	GACGATTAAT	AATGAATCGC	CATTGTTGCT	60
TTCTCCGTTG	TATGGCAATG	ATAATGGTAA	CGGATTATGG	TGGGGGAACA	CATTGAAGGG	120
AGCATGGGAA	GCTATTCTCT	AAGATGTAAA	GCCATATGCA	GCGATTGAAC	TTCATCTGCT	180
AAAAGTCTGT	AAACCAACAA	GTTGTATTCC	ACGAGATACG	AAAGAATTGA	GAGAATGGTA	240
TGTCAAGATG	TTGGAGGAAG	CTCAAAGTCT	AAACATTCCA	GTTTCTTGG	TTATTATGTC	300
GGCTGGAGAG	CGTAATACAG	TTCTCTCCAG	GTGGTTAGAT	GAACAATTCC	AAAAGTATAG	360
TGTGTTAAAA	GGTGTTTTAA	ATATTGAGAA	TTATTGGATT	TACAATAACC	AGTTAGCTCC	420
GCATAGTGCT	AAATATTTGG	AAGTTTGTGC	CAAATATGGA	GCGCATTTTA	TCTGGCATGA	480
TCATGAAAAA	TGGTTCTGGG	AACTATTAT	GAATGATCCG	ACATTCTTTG	AAGCGAGTCA	540
AAAATATCAT	AAAAATTTGG	TGTTGGCAAC	TAAAAATACG	CCAATAAGAG	ATGATGCGGG	600
TACAGATTCT	ATCGTTAGTG	GATTTTGGTT	GAGTGGCTTA	TGTGATAACT	GGGGCTCATC	660
AACAGATACA	TGGAAATGGT	GGGAAAAACA	TTATACAAAC	ACATTTGAAA	CTGGAAGAGC	720
TAGGGATATG	AGATCCTATG	CATCGGAACC	AGAATCAATG	ATTGCTATGG	AAATGATGAA	780
TGTATATACT	GGGGGAGGCA	CAGTTTATAA	TTTCGAATGT	GCCGCGTATA	CATTTATGAC	840
AAATGATGTA	CCAATCCAG	CATTTACTAA	AGGTATTATT	CCTTCTTTA	GACATGCTAT	900
ACAAAATCCA	GCTCCAAGTA	AGGAAGAAGT	TGTAAATAGA	ACAAAAGCTG	TATTTTGGAA	960
TGGAGAAGGT	AGGATTAGTT	CATTAAACGG	ATTTTATCAA	GGACTTTATT	CGAATGATGA	1020
AACAATGCCT	TTATATAATA	ATGGGAGATA	TCATATTCTT	CCTGTAATAC	ATGAGAAAAT	1080
TGATAAGGAA	AAGATTTTAT	CTATATTCCC	TAATGCAAAA	ATTTTGACTA	AAAATAGTGA	1140
GGAATTGTCT	AGTAAAGTCA	ACTATTTAAA	CTCGCTTTAT	CCAAAACTTT	ATGAAGGAGA	1200
TGGGTATGCT	CAGCGTGTAG	GTAATTCCTG	GTATATTTAT	AATAGTAATG	CTAATATCAA	1260
TAAAAATCAG	CAAGTAATGT	TGCCTATGTA	TACTAATAAT	ACAAAGTCGT	TATCGTTAGA	1320
TTTGACGCCA	CATACTTACG	CTGTTGTTAA	AGAAAAATCCA	AATAATTTAC	ATATTTTATT	1380
GAATAATTAC	AGGACAGATA	AGACAGCTAT	GTGGGCATTA	TCAGGAAATT	TTGATGCATC	1440
AAAAAGTTGG	AAGAAAGAAG	AATTAGAGTT	AGCGAACTGG	ATAAGCAAAA	ATTATTCCAT	1500
CAATCCTGTA	GATAATGACT	TTAGGACAAC	AACACTTACA	TTAAAAGGGC	ATACTGGTCA	1560
TAAACCTCAG	ATAAATATAA	GTGGCGATAA	AAATCATTAT	ACTTATACAG	AAAATTGGGA	1620
TGAGAATACC	CATGTTTATA	CCATTACGGT	TAATCATAAT	GGAATGGTAG	AGATGTCTAT	1680
AAATACTGAG	GGGACAGGTC	CAGTCTCTTT	CCCAACACCA	GATAAATTTA	ATGATGGTAA	1740
TTTGAATATA	GCATATGCAA	AACCAACAAC	ACAAAGTTCT	GTAGATTACA	ATGGAGACCC	1800

(2) INFORMATION FOR SEQ ID NO:204:

(A) LENGTH: 657 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:204:

Lys	Ala	Asp	Asn	Arg	Val	Gln	Met	Arg	Thr	Ile	Asn	Asn	Glu	Ser	
1			5					10					15		
Pro	Leu	Leu	Leu	Ser	Pro	Leu	Tyr	Gly	Asn	Asp	Asn	Gly	Asn	Gly	Leu
		20						25				30			
Trp	Trp	Gly	Asn	Thr	Leu	Lys	Gly	Ala	Trp	Glu	Ala	Ile	Pro	Glu	Asp
		35					40					45			
Val	Lys	Pro	Tyr	Ala	Ala	Ile	Glu	Leu	His	Pro	Ala	Lys	Val	Cys	Lys
	50					55					60				
Pro	Thr	Ser	Cys	Ile	Pro	Arg	Asp	Thr	Lys	Glu	Leu	Arg	Glu	Trp	Tyr
65					70					75					80
Val	Lys	Met	Leu	Glu	Glu	Ala	Gln	Ser	Leu	Asn	Ile	Pro	Val	Phe	Leu
				85					90					95	
Val	Ile	Met	Ser	Ala	Gly	Glu	Arg	Asn	Thr	Val	Pro	Pro	Glu	Trp	Leu
			100					105					110		
Asp	Glu	Gln	Phe	Gln	Lys	Tyr	Ser	Val	Leu	Lys	Gly	Val	Leu	Asn	Ile
		115					120					125			
Glu	Asn	Tyr	Trp	Ile	Tyr	Asn	Asn	Gln	Leu	Ala	Pro	His	Ser	Ala	Lys
	130					135					140				
Tyr	Leu	Glu	Val	Cys	Ala	Lys	Tyr	Gly	Ala	His	Phe	Ile	Trp	His	Asp
145					150					155					160
His	Glu	Lys	Trp	Phe	Trp	Glu	Thr	Ile	Met	Asn	Asp	Pro	Thr	Phe	Phe
				165					170					175	
Glu	Ala	Ser	Gln	Lys	Tyr	His	Lys	Asn	Leu	Val	Leu	Ala	Thr	Lys	Asn
			180					185					190		
Thr	Pro	Ile	Arg	Asp	Asp	Ala	Gly	Thr	Asp	Ser	Ile	Val	Ser	Gly	Phe
		195					200					205			
Trp	Leu	Ser	Gly	Leu	Cys	Asp	Asn	Trp	Gly	Ser	Ser	Thr	Asp	Thr	Trp
	210					215					220				
Lys	Trp	Trp	Glu	Lys	His	Tyr	Thr	Asn	Thr	Phe	Glu	Thr	Gly	Arg	Ala

225		230		235		240
Arg Asp Met	Arg Ser Tyr	Ala Ser Glu	Pro Glu Ser	Met Ile Ala	Met	
	245		250		255	
Glu Met Met	Asn Val Tyr	Thr Gly Gly	Gly Thr Val	Tyr Asn Phe	Glu	
	260		265		270	
Cys Ala Ala	Tyr Thr Phe	Met Thr Asn	Asp Val Pro	Thr Pro Ala	Phe	
	275		280		285	
Thr Lys Gly	Ile Ile Pro	Phe Phe Arg	His Ala Ile	Gln Asn Pro	Ala	
	290		295		300	
Pro Ser Lys	Glu Glu Val	Val Asn Arg	Thr Lys Ala	Val Phe Trp	Asn	
305		310		315		320
Gly Glu Gly	Arg Ile Ser	Ser Ser Leu	Asn Gly Phe	Tyr Gln Gly	Leu Tyr	
	325		330		335	
Ser Asn Asp	Glu Thr Met	Pro Leu Tyr	Asn Asn Gly	Arg Tyr His	Ile	
	340		345		350	
Leu Pro Val	Ile His Glu	Lys Ile Asp	Lys Glu Lys	Ile Ser Ser	Ile	
	355		360		365	
Phe Pro Asn	Ala Lys Ile	Leu Thr Lys	Asn Ser Glu	Glu Glu Leu	Ser Ser	
	370		375		380	
Lys Val Asn	Tyr Leu Asn	Ser Leu Tyr	Pro Lys Leu	Tyr Glu Gly	Asp	
385		390		395		400
Gly Tyr Ala	Gln Arg Val	Gly Asn Ser	Trp Tyr Ile	Tyr Asn Ser	Asn	
	405		410		415	
Ala Asn Ile	Asn Lys Asn	Gln Gln Val	Met Leu Pro	Met Tyr Thr	Asn	
	420		425		430	
Asn Thr Lys	Ser Leu Ser	Leu Asp Leu	Thr Pro His	Thr Tyr Ala	Val	
	435		440		445	
Val Lys Glu	Asn Pro Asn	Asn Leu His	Ile Leu Leu	Asn Asn Tyr	Arg	
	450		455		460	
Thr Asp Lys	Thr Ala Met	Trp Ala Leu	Ser Gly Asn	Phe Asp Ala	Ser	
465		470		475		480
Lys Ser Trp	Lys Lys Glu	Glu Glu Leu	Glu Leu Ala	Asn Trp Ile	Ser Lys	
	485		490		495	
Asn Tyr Ser	Ile Asn Pro	Val Asp Asn	Asp Phe Arg	Thr Thr Thr	Leu	
	500		505		510	
Thr Leu Lys	Gly His Thr	Gly His Lys	Pro Gln Ile	Asn Ile Ser	Gly	
	515		520		525	
Asp Lys Asn	His Tyr Thr	Tyr Thr Glu	Asn Trp Asp	Glu Asn Thr	His	
	530		535		540	
Val Tyr Thr	Ile Thr Val	Asn His Asn	Gly Met Val	Glu Met Ser	Ile	
545		550		555		560
Asn Thr Glu	Gly Thr Gly	Pro Val Ser	Phe Pro Thr	Pro Asp Lys	Phe	

09765274 0432004

(2) INFORMATION FOR SEQ ID NO: 205:

(A) LENGTH: 811 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

CTGTGGCAAT	CAGTCAGCTG	CTTCCAAACA	GTGAGCTTCA	GGAACGATTG	AGGTGATTTT	60
ACGAGAAAAT	GGCTCTGGGA	CACGGGGTGC	CTTCACAGAA	ATCACAGGGA	TTCTCAAAAA	120
AGACGGTGAT	AAAAAAATTG	ACAACACTGC	CAAAACAGCT	GTGATTCAAA	ATAGTACAGA	180
AGGTGTTCTC	TCAGCAGTTC	AAGGGAATGC	TAATGCTATC	GGCTACATCT	CCTTGGGATC	240
TTTAACGAAA	TCTGTCAAGG	CTTTAGAGAT	TGATGGTGTC	AAGGCTAGTC	GAGACACAGT	300
TTTAGATGGT	GAATACCCTC	TTCAACGTCC	CTTCAACATT	GTTTGGTCTT	CTAATCTTTC	360
CAAGCTAGGT	CAAGATTTTA	TCAGCTTTAT	CCACTCCAAA	CAAGGTCAAC	AAGTGGTCAC	420
AGATAATAAA	TTTATTGAAG	CTAAAACCGA	AACCACGGAA	TATACAAGCC	AACACTTATC	480
AGGCAAGTTG	TCTGTTGTAG	GTTCCACTTC	AGTATCTTCT	TTAATGGAAA	AATTAGCAGA	540
AGCTTATAAA	AAAGAAAATC	CAGAAGTTAC	GATTGATATT	ACCTCTAATG	GGTCTTCAGC	600
AGGTATTACC	GCTGTTAAGG	AGAAAACCGC	TGATATTGGT	ATGGTTTCTA	GGGAATTAA	660
TCCTGAAGAA	GGTAAGAGTC	TCACCCATGA	TGCTATTGCT	TTAGACGGTA	TTGCTGTTGT	720
GGTCAATAAT	GACAATAAGG	CAAGCCAAGT	CAGTATGGCT	GAACTTGCAG	ACGTTTTTAG	780
TGGCAAATTA	ACCACCTGGG	ACAAGATTAA	A			811

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 270 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:206:

Cys	Gly	Asn	Gln	Ser	Ala	Ala	Ser	Lys	Gln	Ser	Ala	Ser	Gly	Thr	Ile	1	5	10	15
Glu	Val	Ile	Ser	Arg	Glu	Asn	Gly	Ser	Gly	Thr	Arg	Gly	Ala	Phe	Thr	20	25	30	
Glu	Ile	Thr	Gly	Ile	Leu	Lys	Lys	Asp	Gly	Asp	Lys	Lys	Ile	Asp	Asn	35	40	45	
Thr	Ala	Lys	Thr	Ala	Val	Ile	Gln	Asn	Ser	Thr	Glu	Gly	Val	Leu	Ser	50	55	60	
Ala	Val	Gln	Gly	Asn	Ala	Asn	Ala	Ile	Gly	Tyr	Ile	Ser	Leu	Gly	Ser	65	70	75	80
Leu	Thr	Lys	Ser	Val	Lys	Ala	Leu	Glu	Ile	Asp	Gly	Val	Lys	Ala	Ser	85	90	95	
Arg	Asp	Thr	Val	Leu	Asp	Gly	Glu	Tyr	Pro	Leu	Gln	Arg	Pro	Phe	Asn	100	105	110	
Ile	Val	Trp	Ser	Ser	Asn	Leu	Ser	Lys	Leu	Gly	Gln	Asp	Phe	Ile	Ser	115	120	125	
Phe	Ile	His	Ser	Lys	Gln	Gly	Gln	Gln	Val	Val	Thr	Asp	Asn	Lys	Phe	130	135	140	
Ile	Glu	Ala	Lys	Thr	Glu	Thr	Thr	Glu	Tyr	Thr	Ser	Gln	His	Leu	Ser	145	150	155	160
Gly	Lys	Leu	Ser	Val	Val	Gly	Ser	Thr	Ser	Val	Ser	Ser	Leu	Met	Glu	165	170	175	
Lys	Leu	Ala	Glu	Ala	Tyr	Lys	Lys	Glu	Asn	Pro	Glu	Val	Thr	Ile	Asp	180	185	190	
Ile	Thr	Ser	Asn	Gly	Ser	Ser	Ala	Gly	Ile	Thr	Ala	Val	Lys	Glu	Lys	195	200	205	
Thr	Ala	Asp	Ile	Gly	Met	Val	Ser	Arg	Glu	Leu	Thr	Pro	Glu	Glu	Gly	210	215	220	
Lys	Ser	Leu	Thr	His	Asp	Ala	Ile	Ala	Leu	Asp	Gly	Ile	Ala	Val	Val	225	230	235	240
Val	Asn	Asn	Asp	Asn	Lys	Ala	Ser	Gln	Val	Ser	Met	Ala	Glu	Leu	Ala	245	250	255	
Asp	Val	Phe	Ser	Gly	Lys	Leu	Thr	Thr	Trp	Asp	Lys	Ile	Lys	260	265	270			

(2) INFORMATION FOR SEQ ID NO: 207:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 805 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 207:

TTGTCAACAA CAACATGCTA CTTCTGAGGG GACGAATCAA AGGCAAAGCA GTTCAGCGAA 60
 AGTTCCATGG AAAGCTTCAT ACACCAACCT AAACAACCAG GTAAGTACAG AAGAGGTCAA 120
 ATCTCTCTTA TCAGCTCACT TGGATCCAAA TAGTGTGGAT GCATTTTTTA ATCTCGTTAA 180
 TGACTATAAT ACCATTGTCG GCTCAACTGG CTTATCAGGA GATTTCACCT CCTTTACTCA 240
 CACCGAATAC GATGTTGAGA AAATCAGTCA TCTCTGGAAT CAAAAGAAGG GCGATTTTGT 300
 TGGGACCAAC TGCCGTATCA ATAGTTATTG TCTTTTGAAA AATTCAGTCA CCATTCCAAA 360
 GCTTGAAAAG AATGACCAGT TGCTTTTCCT AGATAATGAT GCGATTGATA AAGGAAAGGT 420
 CTTTGATTCA CAAGATAAGG AAGAGTTTGA TATTCTATTT TCGAGAGTTC CAACTGAGTC 480
 AACTACAGAT GTCAAGGTTT ACGCTGAAAA GATGGAAGCA TTCTTCTCAC AATTTCAATT 540
 CAATGAAAAA GCTCGAATGC TGTCTGTAGT CTTGCACGAC AATTTGGATG GCGAGTATCT 600
 GTTTGTAGGC CACGTTGGGG TCTTAGTACC TGCTGATGAC GGTTCCTTAT TTGTAGAGAA 660
 ATTGACTTTC GAAGAGCCCT ACCAAGCGAT TAAATTTGCT AGTAAGGAAG ATTGCTACAA 720
 GTATTTGGGC ACCAAGTATG CGGATTATAC AGGCGAGGGA CTGGCTAAGC CTTTTATCAT 780
 GGATAATGAT AAGTGGGTTA AACTT 805

(2) INFORMATION FOR SEQ ID NO:208:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 268 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:208:

Cys Gln Gln Gln His Ala Thr Ser Glu Gly Thr Asn Gln Arg Gln Ser
 1 5 10 15
 Ser Ser Ala Lys Val Pro Trp Lys Ala Ser Tyr Thr Asn Leu Asn Asn
 20 25 30
 Gln Val Ser Thr Glu Glu Val Lys Ser Leu Leu Ser Ala His Leu Asp
 35 40 45
 Pro Asn Ser Val Asp Ala Phe Phe Asn Leu Val Asn Asp Tyr Asn Thr
 50 55 60

Ile Val Gly Ser Thr Gly Leu Ser Gly Asp Phe Thr Ser Phe Thr His
 65 70 75 80
 Thr Glu Tyr Asp Val Glu Lys Ile Ser His Leu Trp Asn Gln Lys Lys
 85 90 95
 Gly Asp Phe Val Gly Thr Asn Cys Arg Ile Asn Ser Tyr Cys Leu Leu
 100 105 110
 Lys Asn Ser Val Thr Ile Pro Lys Leu Glu Lys Asn Asp Gln Leu Leu
 115 120 125
 Phe Leu Asp Asn Asp Ala Ile Asp Lys Gly Lys Val Phe Asp Ser Gln
 130 135 140
 Asp Lys Glu Glu Phe Asp Ile Leu Phe Ser Arg Val Pro Thr Glu Ser
 145 150 155 160
 Thr Thr Asp Val Lys Val His Ala Glu Lys Met Glu Ala Phe Phe Ser
 165 170 175
 Gln Phe Gln Phe Asn Glu Lys Ala Arg Met Leu Ser Val Val Leu His
 180 185 190
 Asp Asn Leu Asp Gly Glu Tyr Leu Phe Val Gly His Val Gly Val Leu
 195 200 205
 Val Pro Ala Asp Asp Gly Phe Leu Phe Val Glu Lys Leu Thr Phe Glu
 210 215 220
 Glu Pro Tyr Gln Ala Ile Lys Phe Ala Ser Lys Glu Asp Cys Tyr Lys
 225 230 235 240
 Tyr Leu Gly Thr Lys Tyr Ala Asp Tyr Thr Gly Glu Gly Leu Ala Lys
 245 250 255
 Pro Phe Ile Met Asp Asn Asp Lys Trp Val Lys Leu
 260 265

(2) INFORMATION FOR SEQ ID NO: 209:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 508 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 209:

TTGTTTCAGGC AAGTCCGTGA CTAGTGAACA CCAAACGAAA GATGAAATGA AGACGGAGCA 60
 GACAGCTAGT AAAACAAGCG CAGCTAAAGG GAAAGAGGTG GCTGATTTTG AATTGATGGG 120
 AGTAGATGGC AAGACCTACC GTTTATCTGA TTACAAGGGC AAGAAAGTCT ATCTCAAATT 180
 CTGGGCTTCT TGGTGTTCCTA TCTGTCTGGC TAGTCTTCCA GATACGGATG AGATTGCTAA 240
 AGAAGCTGGT GATGACTATG TGGTCTTGAC AGTAGTGTC AAGGACATA AGGGAGAGCA 300
 ATCTGAAGCG GACTTTAAGA ATTGGTATAA GGGATTGGAT TATAAAAATC TCCCAGTCCT 360

AGTTGACCCA TCAGGCAAAC TTTTGGAAAC TTATGGTGTC CGTTCTTACC CAACCCAAGC 420
 CTTTATAGAC AAAGAAGGCA AGCTGGTCAA AACACATCCA GGATTCATGG AAAAAGATGC 480
 AATTTTGCAA ACTTTGAAGG AATTAGCC 508

(2) INFORMATION FOR SEQ ID NO:210:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 169 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:210:

Cys Ser Gly Lys Ser Val Thr Ser Glu His Gln Thr Lys Asp Glu Met
 1 5 10 15
 Lys Thr Glu Gln Thr Ala Ser Lys Thr Ser Ala Ala Lys Gly Lys Glu
 20 25 30
 Val Ala Asp Phe Glu Leu Met Gly Val Asp Gly Lys Thr Tyr Arg Leu
 35 40 45
 Ser Asp Tyr Lys Gly Lys Lys Val Tyr Leu Lys Phe Trp Ala Ser Trp
 50 55 60
 Cys Ser Ile Cys Leu Ala Ser Leu Pro Asp Thr Asp Glu Ile Ala Lys
 65 70 75 80
 Glu Ala Gly Asp Asp Tyr Val Val Leu Thr Val Val Ser Pro Gly His
 85 90 95
 Lys Gly Glu Gln Ser Glu Ala Asp Phe Lys Asn Trp Tyr Lys Gly Leu
 100 105 110
 Asp Tyr Lys Asn Leu Pro Val Leu Val Asp Pro Ser Gly Lys Leu Leu
 115 120 125
 Glu Thr Tyr Gly Val Arg Ser Tyr Pro Thr Gln Ala Phe Ile Asp Lys
 130 135 140
 Glu Gly Lys Leu Val Lys Thr His Pro Gly Phe Met Glu Lys Asp Ala
 145 150 155 160
 Ile Leu Gln Thr Leu Lys Glu Leu Ala
 165

(2) INFORMATION FOR SEQ ID NO: 211:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 994 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 211:

CTCGCAAATT GAAAAGGCGG CAGTTAGCCA AGGAGGAAAA GCAGTGAAAA AACAGAAAT 60
TAGTAAAGAC GCAGACTTGC ACGAAATTTA TCTAGCTGGA GGTGTGTTCT GGGGAGTGGA 120
GGAATATTTT TCACGTGTTT CCGGGGTGAC GGATGCCGTT TCAGGCTATG CAAATGGTAG 180
AGGAGAAACA ACCAAGTACG AATTGATTAA CCAAACAGGT CATGCAGAAA CCGTCCATGT 240
CACCTATGAT GCCAAGCAAA TTTCTCTCAA GGAAATCCTG CTTCACTATT TCCGCATTAT 300
CAATCCAACC AGCAAAAATA AACAAGGAAA TGATGTGGGG ACCCAGTACC GTACTGGTGT 360
TTATTACACA GATGACAAGG ATTTGGAAGT GATTAACCAA GTCTTTGATG AGGTGGCTAA 420
GAAATACGAT CAACCTCTAG CAGTTGAAAA GGAAACTTG AAGAATTTTG TGGTGGCTGA 480
GGATTACCAT CAAGACTATC TCAAGAAAAA TCCAAATGGC TACTGCCATA TCAATGTTAA 540
TCAGGCGGCC TATCCTGTCA TTGATGCCAG CAAATATCCA AAACCAAGTG ATGAGGAATT 600
GAAAAAGACC CTGTCACCTG AGGAGTATGC AGTTACCCAG GAAAATCAAA CAGAACGAGC 660
TTTCTCAAAC CGTTACTGGG ATAAATTTGA ATCCGGTATC TATGTGGATA TAGCAACTGG 720
GGAACCTCTC TTTTCATCAA AAGACAAATT TGAGTCTGGT TGTGGCTGGC CTAGTTTTCAC 780
CCAACCCATC AGTCCAGATG TTGTCACCTA CAAGGAAGAT AAGTCCTACA ATATGACGCG 840
TATGGAAGTG CGGAGCCGAG TAGGAGATTC TCACCTTGGG CATGTCTTTA CGGATGGTCC 900
ACAGGACAAG GCGGGCTTAC GTTACTGTAT CAATAGCCTC TCTATCCGCT TTATTCCCAA 960
AGACCAAATG GAAGAAAAAG GTACGCTTAT TTAC 994

(2) INFORMATION FOR SEQ ID NO:212:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 331 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:212:

Ser Gln Ile Glu Lys Ala Ala Val Ser Gln Gly Gly Lys Ala Val Lys
1 5 10 15
Lys Thr Glu Ile Ser Lys Asp Ala Asp Leu His Glu Ile Tyr Leu Ala
20 25 30
Gly Gly Cys Phe Trp Gly Val Glu Glu Tyr Phe Ser Arg Val Pro Gly
35 40 45
Val Thr Asp Ala Val Ser Gly Tyr Ala Asn Gly Arg Gly Glu Thr Thr
50 55 60
Lys Tyr Glu Leu Ile Asn Gln Thr Gly His Ala Glu Thr Val His Val
65 70 75 80

Thr Tyr Asp Ala Lys Gln Ile Ser Leu Lys Glu Ile Leu Leu His Tyr
 85 90 95
 Phe Arg Ile Ile Asn Pro Thr Ser Lys Asn Lys Gln Gly Asn Asp Val
 100 105 110
 Gly Thr Gln Tyr Arg Thr Gly Val Tyr Tyr Thr Asp Asp Lys Asp Leu
 115 120 125
 Glu Val Ile Asn Gln Val Phe Asp Glu Val Ala Lys Lys Tyr Asp Gln
 130 135 140
 Pro Leu Ala Val Glu Lys Glu Asn Leu Lys Asn Phe Val Val Ala Glu
 145 150 155 160
 Asp Tyr His Gln Asp Tyr Leu Lys Lys Asn Pro Asn Gly Tyr Cys His
 165 170 175
 Ile Asn Val Asn Gln Ala Ala Tyr Pro Val Ile Asp Ala Ser Lys Tyr
 180 185 190
 Pro Lys Pro Ser Asp Glu Glu Leu Lys Lys Thr Leu Ser Pro Glu Glu
 195 200 205
 Tyr Ala Val Thr Gln Glu Asn Gln Thr Glu Arg Ala Phe Ser Asn Arg
 210 215 220
 Tyr Trp Asp Lys Phe Glu Ser Gly Ile Tyr Val Asp Ile Ala Thr Gly
 225 230 235 240
 Glu Pro Leu Phe Ser Ser Lys Asp Lys Phe Glu Ser Gly Cys Gly Trp
 245 250 255
 Pro Ser Phe Thr Gln Pro Ile Ser Pro Asp Val Val Thr Tyr Lys Glu
 260 265 270
 Asp Lys Ser Tyr Asn Met Thr Arg Met Glu Val Arg Ser Arg Val Gly
 275 280 285
 Asp Ser His Leu Gly His Val Phe Thr Asp Gly Pro Gln Asp Lys Gly
 290 295 300
 Gly Leu Arg Tyr Cys Ile Asn Ser Leu Ser Ile Arg Phe Ile Pro Lys
 305 310 315 320
 Asp Gln Met Glu Glu Lys Gly Thr Leu Ile Tyr
 325 330

(2) INFORMATION FOR SEQ ID NO: 213:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 625 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 213:

TTGTCAGTCA GGTTC TAATG GTTCTCAGTC TGCTGTGGAT GCTATCAAAC AAAAAGGGAA 60
 ATTAGTTGTG GCAACCAGTC CTGACTATGC ACCCTTTGAA TTTCAATCAT TGGTTGATGG 120

AAAGAACCAG GTAGTCGGTG CAGACATCGA CATGGCTCAG GCTATCGCTG ATGAACTTGG 180
GGTTAAGTTG GAAATCTCAA GCATGAGTTT TGACAATGTT TTGACCAGTC TTCAAACCTGG 240
TAAGGCTGAC CTAGCAGTTG CAGGAATTAG TGCTACTGAC GAGAGAAAAG AAGTCTTTGA 300
TTTTTCAATC CCATACTATG AAAACAAGAT TAGTTTCTTG GTTCGTAAGG CTGATGTGGA 360
AAAATACAAG GATTTAAC TA GCCTAGAAAAG TGCTAATATT GCAGCCCAAA AAGGGACTGT 420
TCCAGAATCA ATGGTCAAGG AACAATTGCC AAAAGTTCAA TTAACCTCCC TAACTAATAT 480
GGGTGAAGCA GTCAATGAAT TGCAGGCTGG AAAAATAGAT GCTGTTCATA TGGATGAGCC 540
TGTGCACTT AGTTATGCTG CTAAAAACGC TGGCTTAGCT GTCGCAACTG TCAGCTTGAA 600
GATGAAGGAC GGCGACGCCA ATGCC 625

(2) INFORMATION FOR SEQ ID NO:214:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 208 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:214:

Cys	Gln	Ser	Gly	Ser	Asn	Gly	Ser	Gln	Ser	Ala	Val	Asp	Ala	Ile	Lys	1	5	10	15
Gln	Lys	Gly	Lys	Leu	Val	Val	Ala	Thr	Ser	Pro	Asp	Tyr	Ala	Pro	Phe	20	25	30	
Glu	Phe	Gln	Ser	Leu	Val	Asp	Gly	Lys	Asn	Gln	Val	Val	Gly	Ala	Asp	35	40	45	
Ile	Asp	Met	Ala	Gln	Ala	Ile	Ala	Asp	Glu	Leu	Gly	Val	Lys	Leu	Glu	50	55	60	
Ile	Ser	Ser	Met	Ser	Phe	Asp	Asn	Val	Leu	Thr	Ser	Leu	Gln	Thr	Gly	65	70	75	80
Lys	Ala	Asp	Leu	Ala	Val	Ala	Gly	Ile	Ser	Ala	Thr	Asp	Glu	Arg	Lys	85	90	95	
Glu	Val	Phe	Asp	Phe	Ser	Ile	Pro	Tyr	Tyr	Glu	Asn	Lys	Ile	Ser	Phe	100	105	110	
Leu	Val	Arg	Lys	Ala	Asp	Val	Glu	Lys	Tyr	Lys	Asp	Leu	Thr	Ser	Leu	115	120	125	
Glu	Ser	Ala	Asn	Ile	Ala	Ala	Gln	Lys	Gly	Thr	Val	Pro	Glu	Ser	Met	130	135	140	
Val	Lys	Glu	Gln	Leu	Pro	Lys	Val	Gln	Leu	Thr	Ser	Leu	Thr	Asn	Met	145	150	155	160
Gly	Glu	Ala	Val	Asn	Glu	Leu	Gln	Ala	Gly	Lys	Ile	Asp	Ala	Val	His				

165

170

175

Met Asp Glu Pro Val Ala Leu Ser Tyr Ala Ala Lys Asn Ala Gly Leu
 180 185 190

Ala Val Ala Thr Val Ser Leu Lys Met Lys Asp Gly Asp Ala Asn Ala
 195 200 205

(2) INFORMATION FOR SEQ ID NO: 215:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3022 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 215:

GGAAACTTCA CAGGATTTTA AAGAGAAGAA AACAGCAGTC ATTAAGGAAA AAGAAGTTGT	60
TAGTAAAAAT CCTGTGATAG ACAATAACAC TAGCAATGAA GAAGCAAAAA TCAAAGAAGA	120
AAATTCCAAT AAATCCCAAG GAGATTATAC GGACTCATT GTGAATAAAA ACACAGAAAA	180
TCCCCAAAAA GAAGATAAAG TTGTCTATAT TGCTGAATTT AAAGATAAAG AATCTGGAGA	240
AAAAGCAATC AAGGAAC TAT CCAGTCTTAA GAATACAAAA GTTTTATATA CTTATGATAG	300
AATTTTAAAC GGTAGTGCCA TAGAAACAAC TCCAGATAAC TTGGACAAAA TTAAACAAAT	360
AGAAGGTATT TCATCGGTTG AAAGGGCACA AAAAGTCCAA CCCATGATGA ATCATGCCAG	420
AAAGGAAATT GGAGTTGAGG AAGCTATTGA TTACCTAAAG TCTATCAATG CTCCGTTTGG	480
GAAAAATTTT GATGGTAGAG GTATGGTCAT TTCAAATATC GATACTGGAA CAGATTATAG	540
ACATAAGGCT ATGAGAATCG ATGATGATGC CAAAGCCTCA ATGAGATTTA AAAAAGAAGA	600
CTTAAAAGGC ACTGATAAAA ATTATTGGTT GAGTGATAAA ATCCCTCATG CGTTCAATTA	660
TTATAATGGT GGCAAAATCA CTGTAGAAAA ATATGATGAT GGAAGGGATT ATTTTGACCC	720
ACATGGGATG CATATTGCAG GGATTCTTGC TGGAAATGAT ACTGAACAAG ACATCAAAAA	780
CTTTAACGGC ATAGATGGAA TTGCACCTAA TGCACAAATT TTCTCTTACA AAATGTATTC	840
TGACGCAGGA TCTGGGTTTG CGGGTGATGA AACAATGTTT CATGCTATTG AAGATTCTAT	900
CAAACACAAC GTTGATGTTG TTTCGGTATC ATCTGGTTTT ACAGGAACAG GTCTTG TAGG	960
TGAGAAATAT TGGCAAGCTA TTCGGGCATT AAGAAAAGCA GGCATTCCAA TGGTTGTCGC	1020
TACGGGTAAC TATGCGACTT CTGCTTCAAG TTCTTCATGG GATTTAGTAG CAAATAATCA	1080
TCTGAAATG ACCGACACTG GAAATGTAAC ACGAACTGCA GCACATGAAG ATGCGATAGC	1140
GGTCGCTTCT GCTAAAAATC AAACAGTTGA GTTTGATAAA GTTAACATAG GTGGAGAAAG	1200
TTTTAAATAC AGAAATATAG GGGCCTTTTT CGATAAGAGT AAAATCACAA CAAATGAAGA	1260
TGGAACAAAA GCTCCTAGTA AATTAAATTT TGTATATATA GGCAAGGGGC AAGACCAAGA	1320

TTTGATAGGT TTGGATCTTA GGGGCAAAAT TGCAGTAATG GATAGAATTT ATACAAAGGA 1380
 TTTAAAAAAT GCTTTTAAAA AAGCTATGGA TAAGGGTGCA CGCGCCATTA TGGTTGTAAA 1440
 TACTGTAAAT TACTACAATA GAGATAATTG GACAGAGCTT CCAGCTATGG GATATGAAGC 1500
 GGATGAAGGT ACTAAAAGTC AAGTGTTTTT AATTTTCAGGA GATGATGGTG TAAAGCTATG 1560
 GAACATGATT AATCCTGATA AAAAACTGA AGTCAAAAGA AATAATAAAG AAGATTTTAA 1620
 AGATAAATTG GAGCAATACT ATCCAATTGA TATGGAAAGT TTTAATTCCA ACAAACCGAA 1680
 TGTAGGTGAC GAAAAAGAGA TTGACTTTAA GTTTGCACCT GACACAGACA AAGAACTCTA 1740
 TAAAGAAGAT ATCATCGTTC CAGCAGGATC TACATCTTGG GGGCCAAGAA TAGATTTACT 1800
 TTTAAAACCC GATGTTTCAG CACCTGGTAA AAATATTAAA TCCACGCTTA ATGTTATTAA 1860
 TGGCAAATCA ACTTATGGCT ATATGTCAGG AACTAGTATG GCGACTCCAA TCGTGGCAGC 1920
 TTCTACTGTT TTGATTAGAC CGAAATTAAA GGAAATGCTT GAAAGACCTG TATTGAAAAA 1980
 TCTTAAGGGA GATGACAAAA TAGATCTTAC AAGTCTTACA AAAATTGCCC TACAAAATAC 2040
 TGCGCGACCT ATGATGGATG CAACTTCTTG GAAAGAAAAA AGTCAATACT TTGCATCACC 2100
 TAGACAACAG GGAGCAGGCC TAATTAATGT GGCCAATGCT TTGAGAAATG AAGTTGTAGC 2160
 AACTTTCAAA AACACTGATT CTAAAGGTTT GGTAAACTCA TATGGTTCCA TTTCTCTTAA 2220
 AGAAATAAAA GGTGATAAAA AATACTTTAC AATCAAGCTT CACAATACAT CAAACAGACC 2280
 TTTGACTTTT AAAGTTTCAG CATCAGCGAT AACTACAGAT TCTCTAACTG ACAGATTAAA 2340
 ACTTGATGAA ACATATAAAG ATGAAAAATC TCCAGATGGT AAGCAAATTG TTCCAGAAAT 2400
 TCACCCAGAA AAAGTCAAAG GAGCAAATAT CACATTTGAG CATGATACTT TCACTATAGG 2460
 CGCAAATTCT AGCTTTGATT TGAATGCGGT TATAAATGTT GGAGAGGCCA AAAACAAAAA 2520
 TAAATTTGTA GAATCATTTA TTCATTTTGA GTCAGTGGA GCGATGGAAG CTCTAAACTC 2580
 CAGCGGGAAG AAAATAAACT TCCAACCTTC TTTGTCGATG CCTCTAATGG GATTTGCTGG 2640
 GAATTGGAAC CACGAACCAA TCCTTGATAA ATGGGCTTGG GAAGAAGGGT CAAGATCAAA 2700
 AACACTGGGA GGTATATGATG ATGATGGTAA ACCGAAAATT CCAGGAACCT TAAATAAGGG 2760
 AATTGGTGGA GAACATGGTA TAGATAAATT TAATCCAGCA GGAGTTATAC AAAATAGAAA 2820
 AGATAAAAAT ACAACATCCC TGGATCAAAA TCCAGAATTA TTTGCTTTCA ATAACGAAGG 2880
 GATCAACGCT CCATCATCAA GTGGTTCTAA GATTGCTAAC ATTTATCCTT TAGATTCAAA 2940
 TGGAAATCCT CAAGATGCTC AACTTGAAAG AGGATTAACA CCTTCTCCAC TTGTATTAAG 3000
 AAGTGCAGAA GAAGGATTGA TT 3022

(2) INFORMATION FOR SEQ ID NO:216:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1007 amino acids

00765274.013904

- (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:216:

Glu	Thr	Ser	Gln	Asp	Phe	Lys	Glu	Lys	Lys	Thr	Ala	Val	Ile	Lys	Glu	1	5	10	15
Lys	Glu	Val	Val	Ser	Lys	Asn	Pro	Val	Ile	Asp	Asn	Asn	Thr	Ser	Asn	20	25	30	
Glu	Glu	Ala	Lys	Ile	Lys	Glu	Glu	Asn	Ser	Asn	Lys	Ser	Gln	Gly	Asp	35	40	45	
Tyr	Thr	Asp	Ser	Phe	Val	Asn	Lys	Asn	Thr	Glu	Asn	Pro	Lys	Lys	Glu	50	55	60	
Asp	Lys	Val	Val	Tyr	Ile	Ala	Glu	Phe	Lys	Asp	Lys	Glu	Ser	Gly	Glu	65	70	75	80
Lys	Ala	Ile	Lys	Glu	Leu	Ser	Ser	Leu	Lys	Asn	Thr	Lys	Val	Leu	Tyr	85	90	95	
Thr	Tyr	Asp	Arg	Ile	Phe	Asn	Gly	Ser	Ala	Ile	Glu	Thr	Thr	Pro	Asp	100	105	110	
Asn	Leu	Asp	Lys	Ile	Lys	Gln	Ile	Glu	Gly	Ile	Ser	Ser	Val	Glu	Arg	115	120	125	
Ala	Gln	Lys	Val	Gln	Pro	Met	Met	Asn	His	Ala	Arg	Lys	Glu	Ile	Gly	130	135	140	
Val	Glu	Glu	Ala	Ile	Asp	Tyr	Leu	Lys	Ser	Ile	Asn	Ala	Pro	Phe	Gly	145	150	155	160
Lys	Asn	Phe	Asp	Gly	Arg	Gly	Met	Val	Ile	Ser	Asn	Ile	Asp	Thr	Gly	165	170	175	
Thr	Asp	Tyr	Arg	His	Lys	Ala	Met	Arg	Ile	Asp	Asp	Asp	Ala	Lys	Ala	180	185	190	
Ser	Met	Arg	Phe	Lys	Lys	Glu	Asp	Leu	Lys	Gly	Thr	Asp	Lys	Asn	Tyr	195	200	205	
Trp	Leu	Ser	Asp	Lys	Ile	Pro	His	Ala	Phe	Asn	Tyr	Tyr	Asn	Gly	Gly	210	215	220	
Lys	Ile	Thr	Val	Glu	Lys	Tyr	Asp	Asp	Gly	Arg	Asp	Tyr	Phe	Asp	Pro	225	230	235	240
His	Gly	Met	His	Ile	Ala	Gly	Ile	Leu	Ala	Gly	Asn	Asp	Thr	Glu	Gln	245	250	255	
Asp	Ile	Lys	Asn	Phe	Asn	Gly	Ile	Asp	Gly	Ile	Ala	Pro	Asn	Ala	Gln	260	265	270	
Ile	Phe	Ser	Tyr	Lys	Met	Tyr	Ser	Asp	Ala	Gly	Ser	Gly	Phe	Ala	Gly	275	280	285	

City	Eys	ASH	HS	Eys	Scr	HS	Edu	ASH	Var	HS	ASH	City	Eys	Scr	HS
610						615						620			

Tyr Gly Tyr Met Ser Gly Thr Ser Met Ala Thr Pro Ile Val Ala Ala
 625 630 635 640
 Ser Thr Val Leu Ile Arg Pro Lys Leu Lys Glu Met Leu Glu Arg Pro
 645 650 655
 Val Leu Lys Asn Leu Lys Gly Asp Asp Lys Ile Asp Leu Thr Ser Leu
 660 665 670
 Thr Lys Ile Ala Leu Gln Asn Thr Ala Arg Pro Met Met Asp Ala Thr
 675 680 685
 Ser Trp Lys Glu Lys Ser Gln Tyr Phe Ala Ser Pro Arg Gln Gln Gly
 690 695 700
 Ala Gly Leu Ile Asn Val Ala Asn Ala Leu Arg Asn Glu Val Val Ala
 705 710 715 720
 Thr Phe Lys Asn Thr Asp Ser Lys Gly Leu Val Asn Ser Tyr Gly Ser
 725 730 735
 Ile Ser Leu Lys Glu Ile Lys Gly Asp Lys Lys Tyr Phe Thr Ile Lys
 740 745 750
 Leu His Asn Thr Ser Asn Arg Pro Leu Thr Phe Lys Val Ser Ala Ser
 755 760 765
 Ala Ile Thr Thr Asp Ser Leu Thr Asp Arg Leu Lys Leu Asp Glu Thr
 770 775 780
 Tyr Lys Asp Glu Lys Ser Pro Asp Gly Lys Gln Ile Val Pro Glu Ile
 785 790 795 800
 His Pro Glu Lys Val Lys Gly Ala Asn Ile Thr Phe Glu His Asp Thr
 805 810 815
 Phe Thr Ile Gly Ala Asn Ser Ser Phe Asp Leu Asn Ala Val Ile Asn
 820 825 830
 Val Gly Glu Ala Lys Asn Lys Asn Lys Phe Val Glu Ser Phe Ile His
 835 840 845
 Phe Glu Ser Val Glu Ala Met Glu Ala Leu Asn Ser Ser Gly Lys Lys
 850 855 860
 Ile Asn Phe Gln Pro Ser Leu Ser Met Pro Leu Met Gly Phe Ala Gly
 865 870 875 880
 Asn Trp Asn His Glu Pro Ile Leu Asp Lys Trp Ala Trp Glu Glu Gly
 885 890 895
 Ser Arg Ser Lys Thr Leu Gly Gly Tyr Asp Asp Asp Gly Lys Pro Lys
 900 905 910
 Ile Pro Gly Thr Leu Asn Lys Gly Ile Gly Gly Glu His Gly Ile Asp
 915 920 925
 Lys Phe Asn Pro Ala Gly Val Ile Gln Asn Arg Lys Asp Lys Asn Thr
 930 935 940
 Thr Ser Leu Asp Gln Asn Pro Glu Leu Phe Ala Phe Asn Asn Glu Gly
 945 950 955 960

102210-1-655260
 102210-1-655260
 102210-1-655260

Ile Asn Ala Pro Ser Ser Ser Gly Ser Lys Ile Ala Asn Ile Tyr Pro
965 970 975

Leu Asp Ser Asn Gly Asn Pro Gln Asp Ala Gln Leu Glu Arg Gly Leu
980 985 990

Thr Pro Ser Pro Leu Val Leu Arg Ser Ala Glu Glu Gly Leu Ile
995 1000 1005

(2) INFORMATION FOR SEQ ID NO: 217:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1696 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 217:

TGTGGTCGAA GTTGAGACTC CTCAATCAAT AACAAATCAG GAGCAAGCTA GGACAGAAAA	60
CCAAGTAGTA GAGACAGAGG AAGCTCCAAA AGAAGAAGCA CCTAAAACAG AAGAAAGTCC	120
AAAGGAAGAA CCAAATCGG AGGTAAACC TACTGACGAC ACCCTTCCTA AAGTAGAAGA	180
GGGGAAGAA GATTGAGCAG AACCAGCTCC AGTTGAAGAA GTAGGTGGAG AAGTTGAGTC	240
AAAACCAGAG GAAAAAGTAG CAGTTAAGCC AGAAAGTCAA CCATCAGACA AACCAGCTGA	300
GGAATCAAAA GTTGAACAAG CAGGTGAACC AGTCGCGCCA AGAGAAGACG AAAAGGCACC	360
AGTCGAGCCA GAAAGCAAC CAGAAGCTCC TGAAGAAGAG AAGGCTGTAG AGGAAACACC	420
GAAACAAGAA GAGTCAACTC CAGATACCAA GGCTGAAGAA ACTGTAGAAC CAAAAGAGGA	480
GACTGTTAAT CAATCTATTG AACAACCAA AGTTGAAACG CCTGCTGTAG AAAACAAAC	540
AGAACCAACA GAGGAACCAA AAGTTGAACA AGCAGGTGAA CCAGTCGCGC CAAGAGAAGA	600
CGAAGAGGCA CCAACGGCAG CAGTTGAGCC AGAAAAGCAA CCAGAAGTTC CTGAAGAAGA	660
GAAGGCTGTA GAGGAAACAC CGAAACCAGA AGATAAAATA AAGGGTATTG GTACTAAAGA	720
ACCAGTTGAT AAAAGTGAGT TAAATAATCA AATTGATAAA GCTAGTTCAG TTTCTCCTAC	780
TGATTATTCT ACAGCAAGTT ACAATGCTCT TGGACCTGTT TTAGAAACTG CAAAAGGTGT	840
CTATGCTTCA GAGCCTGTAA AACAGCCTGA GGTAAATAGC GAGACAAATA AACTTAAAC	900
GGCTATTGAC GCTCTAAACG TTGATAAAAC TGAATTAAAC AATACGATTG CAGATGCAAA	960
AACAAAGGTA AAAGAACATT ACAGTGATAG AAGTTGGCAA AACCTCCAAA CTGAAGTTAC	1020
AAAGGCTGAA AAAGTTGCAG CTAATACAGA TGCTAAACAA AGTGAAGTTA ACGAAGCTGT	1080
TGAAAAATTA ACTGCAACTA TTGAAAAATT GGTGAATTA TCTGAAAAGC CAATATTAAC	1140
ATTGACTAGT ACCGATAAGA AAATATTGGA ACGTGAAGCT GTTGCTAAGT ATACTCTAGA	1200
AAATCAAAAC AAAACAAAA TCAAATCAAT CACAGCTGAA TTGAAAAAG GAGAAGAAGT	1260

TATTAATACT GTAGTCCTTA CAGATGACAA GGTAACAACA GAAACTATAA GCGCTGCATT 1320
 TAAGAACCTA GAGTACTACA AAGAATACAC CCTATCTACA ACTATGATTT ACGACAGAGG 1380
 TAACGGTGAA GAAACTGAAA CTCTAGAAAA TCAAAATATT CAATTAGATC TTAAAAAAGT 1440
 TGAGCTTAAA AATATTAAAC GTACAGATTT AATCAAATAC GAAAATGGAA AAGAAACTAA 1500
 TGAATCACTG ATAACAATA TTCCTGATGA TAAGAGCAAT TATTATTTAA AAATAACTTC 1560
 AAATAATCAG AAAACTACAT TACTAGCTGT TAAAAATATA GAAGAAACTA CGGTAAACGG 1620
 AACACCTGTA TATAAAGTTA CAGCAATCGC AGACAATTTA GTCTCTAGAA CTGCTGATAA 1680
 TAAATTTGAA GAAGAA 1696

(2) INFORMATION FOR SEQ ID NO:218:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 565 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:218:

Val	Val	Glu	Val	Glu	Thr	Pro	Gln	Ser	Ile	Thr	Asn	Gln	Glu	Gln	Ala	1	5	10	15
Arg	Thr	Glu	Asn	Gln	Val	Val	Glu	Thr	Glu	Glu	Ala	Pro	Lys	Glu	Glu	20	25	30	
Ala	Pro	Lys	Thr	Glu	Glu	Ser	Pro	Lys	Glu	Glu	Pro	Lys	Ser	Glu	Val	35	40	45	
Lys	Pro	Thr	Asp	Asp	Thr	Leu	Pro	Lys	Val	Glu	Glu	Gly	Lys	Glu	Asp	50	55	60	
Ser	Ala	Glu	Pro	Ala	Pro	Val	Glu	Glu	Val	Gly	Gly	Glu	Val	Glu	Ser	65	70	75	80
Lys	Pro	Glu	Glu	Lys	Val	Ala	Val	Lys	Pro	Glu	Ser	Gln	Pro	Ser	Asp	85	90	95	
Lys	Pro	Ala	Glu	Glu	Ser	Lys	Val	Glu	Gln	Ala	Gly	Glu	Pro	Val	Ala	100	105	110	
Pro	Arg	Glu	Asp	Glu	Lys	Ala	Pro	Val	Glu	Pro	Glu	Lys	Gln	Pro	Glu	115	120	125	
Ala	Pro	Glu	Glu	Glu	Lys	Ala	Val	Glu	Glu	Thr	Pro	Lys	Gln	Glu	Glu	130	135	140	
Ser	Thr	Pro	Asp	Thr	Lys	Ala	Glu	Glu	Thr	Val	Glu	Pro	Lys	Glu	Glu	145	150	155	160
Thr	Val	Asn	Gln	Ser	Ile	Glu	Gln	Pro	Lys	Val	Glu	Thr	Pro	Ala	Val	165	170	175	
Glu	Lys	Gln	Thr	Glu	Pro	Thr	Glu	Glu	Pro	Lys	Val	Glu	Gln	Ala	Gly				

180					185					190				
Glu	Pro	Val	Ala	Pro	Arg	Glu	Asp	Glu	Gln	Ala	Pro	Thr	Ala	Pro
195							200					205		
Glu	Pro	Glu	Lys	Gln	Pro	Glu	Val	Pro	Glu	Glu	Glu	Lys	Ala	Val
210					215					220				Glu
Glu	Thr	Pro	Lys	Pro	Glu	Asp	Lys	Ile	Lys	Gly	Ile	Gly	Thr	Lys
225					230					235				240
Pro	Val	Asp	Lys	Ser	Glu	Leu	Asn	Asn	Gln	Ile	Asp	Lys	Ala	Ser
				245					250				255	Ser
Val	Ser	Pro	Thr	Asp	Tyr	Ser	Thr	Ala	Ser	Tyr	Asn	Ala	Leu	Gly
			260					265					270	Pro
Val	Leu	Glu	Thr	Ala	Lys	Gly	Val	Tyr	Ala	Ser	Glu	Pro	Val	Lys
			275				280					285		Gln
Pro	Glu	Val	Asn	Ser	Glu	Thr	Asn	Lys	Leu	Lys	Thr	Ala	Ile	Asp
290					295					300				Ala
Leu	Asn	Val	Asp	Lys	Thr	Glu	Leu	Asn	Asn	Thr	Ile	Ala	Asp	Lys
305					310					315				320
Thr	Lys	Val	Lys	Glu	His	Tyr	Ser	Asp	Arg	Ser	Trp	Gln	Asn	Gln
				325					330				335	
Thr	Glu	Val	Thr	Lys	Ala	Glu	Lys	Val	Ala	Ala	Asn	Thr	Asp	Lys
			340					345					350	
Gln	Ser	Glu	Val	Asn	Glu	Ala	Val	Glu	Lys	Leu	Thr	Ala	Thr	Ile
			355				360					365		Glu
Lys	Leu	Val	Glu	Leu	Ser	Glu	Lys	Pro	Ile	Leu	Thr	Leu	Thr	Ser
			370			375					380			Thr
Asp	Lys	Lys	Ile	Leu	Glu	Arg	Glu	Ala	Val	Ala	Lys	Tyr	Thr	Glu
385					390					395				400
Asn	Gln	Asn	Lys	Thr	Lys	Ile	Lys	Ser	Ile	Thr	Ala	Glu	Leu	Lys
				405					410				415	Lys
Gly	Glu	Glu	Val	Ile	Asn	Thr	Val	Val	Leu	Thr	Asp	Asp	Lys	Val
			420					425					430	Thr
Thr	Glu	Thr	Ile	Ser	Ala	Ala	Phe	Lys	Asn	Leu	Glu	Tyr	Tyr	Lys
			435				440					445		Glu
Tyr	Thr	Leu	Ser	Thr	Thr	Met	Ile	Tyr	Asp	Arg	Gly	Asn	Gly	Glu
					455					460				Glu
Thr	Glu	Thr	Leu	Glu	Asn	Gln	Asn	Ile	Gln	Leu	Asp	Leu	Lys	Val
465					470					475				480
Glu	Leu	Lys	Asn	Ile	Lys	Arg	Thr	Asp	Leu	Ile	Lys	Tyr	Glu	Gly
				485					490				495	
Lys	Glu	Thr	Asn	Glu	Ser	Leu	Ile	Thr	Thr	Ile	Pro	Asp	Asp	Ser
			500					505					510	
Asn	Tyr	Tyr	Leu	Lys	Ile	Thr	Ser	Asn	Asn	Gln	Lys	Thr	Thr	Leu
														Leu

515 520 525
 Ala Val Lys Asn Ile Glu Glu Thr Thr Val Asn Gly Thr Pro Val Tyr
 530 535 540
 Lys Val Thr Ala Ile Ala Asp Asn Leu Val Ser Arg Thr Ala Asp Asn
 545 550 555 560
 Lys Phe Glu Glu Glu
 565

(2) INFORMATION FOR SEQ ID NO: 219:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1879 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 219:

AACACCTGTA TATAAAGTTA CAGCAATCGC AGACAATTTA GTCTCTAGAA CTGCTGATAA	60
TAAATTTGAA GAAGAATACG TTCACTATAT TGAAAAACCT AAAGTCCACG AAGATAATGT	120
ATATTATAAT TTCAAAGAAT TAGTGGAAGC TATTCAAAAC GATCCTTCAA AAGAATATCG	180
TCTGGGACAA TCAATGAGCG CTAGAAATGT TGTTCCTAAT GGAAAATCAT ATATCACTAA	240
AGAATTCACA GGAAACTTTT TAAGTTCTGA AGGAAAACAA TTTGCTATTA CTGAATTGGA	300
ACATCCATTA TTTAATGTGA TAACAAACGC AACGATAAAT AATGTGAATT TTGAAAATGT	360
AGAGATAGAA CGTTCTGGTC AAGATAATAT TGCATCATTG GCCAATACTA TGAAAGGTTC	420
TTCAAGTTATT ACAAATGTCA AAATTACAGG CACACTTTCA GGTCGTAATA ATGTTGCTGG	480
ATTTGTAAAT AATATGAATG ATGGAACCTG TATTGAAAAT GTTGCTTTCT TTGGCAAACCT	540
ACACTCTACA AGTGGAAATG GCTCTCATAC AGGGGGAATT GCAGGTACAA ACTATAGAGG	600
AATTGTTAGA AAAGCATATG TTGATGCTAC TATTACAGGA AACAAAACAC GCGCCAGCTT	660
GTTAGTTCCT AAAGTAGATT ATGGATTAAC TCTAGACCAT CTTATTGGTA CAAAAGCTCT	720
CCTAACTGAG TCGGTTGTAA AAGGTAAAAT AGATGTTTCA AATCCAGTAG AAGTTGGAGC	780
AATAGCAAGT AAGACTTGGC CTGTAGGTAC GGTAAGTAAT TCTGTCAGCT ATGCTAAGAT	840
TATCCGTGGA GAGGAGTTAT TCGGCTCTAA CGACGTTGAT GATTCTGATT ATGCTAGTGC	900
TCATATAAAA GATTTATATG CGGTAGAGGG ATATTCGTCA GGTAATAGAT CATTTAGGAA	960
ATCTAAACAA TTTACTAAAT TAACTAAAGA ACAAGCTGAT GCTAAAGTTA CTACTTTCAA	1020
TATTACTGCT GATAAATTAG AAAGTGATCT ATCTCCTCTT GCAAAACTTA ATGAAGAAAA	1080
AGCCTATTCT AGTATTCAAG ATTATAACGC TGAATATAAC CAAGCCTATA AAAATCTTGA	1140
AAAATTAATA CCATTCTACA ATAAAGATTA TATTGTATAT CAAGGTAATA AATTAAATAA	1200

AGAACACCAT CTAAATACTA AAGAAGTTCT TTCTGTTACC GCGATGAACA ACAATGAGTT 1260
 TATCACAAAC CTAGATGAAG CTAATAAAAT TATTGTTTAC TATGCGGACG GTACAAAAGA 1320
 TTACTTTAAC TTGTCTTCTA GCAGTGAAGG TTTAAGTAAT GTAAAAGAAT ATACTATAAC 1380
 TGACTIONAGGA ATTAAATATA CACCTAATAT CGTTCAAAAA GATAACACTA CTCTTGTTAA 1440
 TGATATAAAA TCTATTTTAG AATCAGTAGA GCTTCAGTCT CAAACGATGT ATCAGCATCT 1500
 AAATCGATTA GGTGACTATA GAGTTAATGC AATCAAAGAT TTATATTTAG AAGAAAGCTT 1560
 CACAGATGTT AAAGAAAACCT TAACAAACCT AATCACAAAA TTAGTTCAAA ACGAAGAACA 1620
 TCAACTAAAT GATTCTCCAG CTGCTCGTCA AATGATTCGT GATAAAGTCG AGAAAAACAA 1680
 AGCAGCTTTA TTACTAGGTT TAACTTACCT AAATCGTTAC TATGGAGTTA AATTTGGTGA 1740
 TGTTAATATT AAAGAATTAA TGCTATTCAA ACCAGATTTT TATGGTGAAA AAGTTAGCGT 1800
 ATTAGACAGA TTAATTGAAA TCGGTTCTAA AGAGAACAAC ATTAAAGGTT CACGTACATT 1860
 CGACGCATTC GGTCAAGTA 1879

(2) INFORMATION FOR SEQ ID NO:220:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 626 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:220:

Thr	Pro	Val	Tyr	Lys	Val	Thr	Ala	Ile	Ala	Asp	Asn	Leu	Val	Ser	Arg
1				5					10					15	
Thr	Ala	Asp	Asn	Lys	Phe	Glu	Glu	Glu	Tyr	Val	His	Tyr	Ile	Glu	Lys
			20					25					30		
Pro	Lys	Val	His	Glu	Asp	Asn	Val	Tyr	Tyr	Asn	Phe	Lys	Glu	Leu	Val
		35					40					45			
Glu	Ala	Ile	Gln	Asn	Asp	Pro	Ser	Lys	Glu	Tyr	Arg	Leu	Gly	Gln	Ser
		50				55					60				
Met	Ser	Ala	Arg	Asn	Val	Val	Pro	Asn	Gly	Lys	Ser	Tyr	Ile	Thr	Lys
65					70				75					80	
Glu	Phe	Thr	Gly	Lys	Leu	Leu	Ser	Ser	Glu	Gly	Lys	Gln	Phe	Ala	Ile
			85					90					95		
Thr	Glu	Leu	Glu	His	Pro	Leu	Phe	Asn	Val	Ile	Thr	Asn	Ala	Thr	Ile
		100						105					110		
Asn	Asn	Val	Asn	Phe	Glu	Asn	Val	Glu	Ile	Glu	Arg	Ser	Gly	Gln	Asp
		115					120					125			
Asn	Ile	Ala	Ser	Leu	Ala	Asn	Thr	Met	Lys	Gly	Ser	Ser	Val	Ile	Thr
		130					135					140			

Asp Ile Lys Ser Ile Leu Glu Ser Val Glu Leu Gln Ser Gln Thr Met
 485 490 495
 Tyr Gln His Leu Asn Arg Leu Gly Asp Tyr Arg Val Asn Ala Ile Lys
 500 505 510
 Asp Leu Tyr Leu Glu Glu Ser Phe Thr Asp Val Lys Glu Asn Leu Thr
 515 520 525
 Asn Leu Ile Thr Lys Leu Val Gln Asn Glu Glu His Gln Leu Asn Asp
 530 535 540
 Ser Pro Ala Ala Arg Gln Met Ile Arg Asp Lys Val Glu Lys Asn Lys
 545 550 555 560
 Ala Ala Leu Leu Leu Gly Leu Thr Tyr Leu Asn Arg Tyr Tyr Gly Val
 565 570 575
 Lys Phe Gly Asp Val Asn Ile Lys Glu Leu Met Leu Phe Lys Pro Asp
 580 585 590
 Phe Tyr Gly Glu Lys Val Ser Val Leu Asp Arg Leu Ile Glu Ile Gly
 595 600 605
 Ser Lys Glu Asn Asn Ile Lys Gly Ser Arg Thr Phe Asp Ala Phe Gly
 610 615 620
 Gln Val
 625

(2) INFORMATION FOR SEQ ID NO: 221:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1777 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 221:

ATTAGACAGA TTAATTGAAA TCGGTTCTAA AGAGAACAAC ATTAAAGGTT CACGTACATT	60
CGACGCATTC GGTCAAGTAT TGGCTAAATA TACTAAATCA GGTAATTTAG ATGCATTTTT	120
AAATTATAAT AGACAATTGT TCACAAATAT AGACAATATG AACGATTGGT TTATTGATGC	180
TACAGAAGAC CATGTCTACA TCGCAGAACG CGCTTCTGAG GTCGAAGAAA TAAAAAATTC	240
TAAACATCGT GCATTCGATA ATTTAAAACG AAGTCACCTT AGAAATACTA TACTCCCACT	300
ACTGAATATT GATAAAGCAC ATCTTTATTT AATTTCAAAT TATAATGCAA TTGCCCTTGG	360
TAGTGCAGAG CGATTAGGTA AAAAATCATT AGAAGATATT AAAGATATCG TTAACAAAGC	420
TGCAGATGGT TATAGAAACT ATTATGATTT CTGGTATCGT CTAGCGTCTG ATAACGTTAA	480
ACAACGACTA CTAAGAGATG CTGTTATTCC TATTTGGGAA GGTATAACG CTCCTGGTGG	540
ATGGGTTGAA AAATATGGCC GCTATAATAC CGACAAAGTA TATACTCCTC TTAGAGAATT	600

(2) INFORMATION FOR SEQ ID NO:222:

(A) LENGTH: 592 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:222:

Asn Ile Asp Asn Met Asn Asp Trp Phe Ile Asp Ala Thr Glu Asp His

50

55

60

Val Tyr Ile Ala Glu Arg Ala Ser Glu Val Glu Glu Ile Lys Asn Ser
 65 70 75 80
 Lys His Arg Ala Phe Asp Asn Leu Lys Arg Ser His Leu Arg Asn Thr
 85 90 95
 Ile Leu Pro Leu Leu Asn Ile Asp Lys Ala His Leu Tyr Leu Ile Ser
 100 105 110
 Asn Tyr Asn Ala Ile Ala Phe Gly Ser Ala Glu Arg Leu Gly Lys Lys
 115 120 125
 Ser Leu Glu Asp Ile Lys Asp Ile Val Asn Lys Ala Ala Asp Gly Tyr
 130 135 140
 Arg Asn Tyr Tyr Asp Phe Trp Tyr Arg Leu Ala Ser Asp Asn Val Lys
 145 150 155 160
 Gln Arg Leu Leu Arg Asp Ala Val Ile Pro Ile Trp Glu Gly Tyr Asn
 165 170 175
 Ala Pro Gly Gly Trp Val Glu Lys Tyr Gly Arg Tyr Asn Thr Asp Lys
 180 185 190
 Val Tyr Thr Pro Leu Arg Glu Phe Phe Gly Pro Met Asp Lys Tyr Tyr
 195 200 205
 Asn Tyr Asn Gly Thr Gly Ala Tyr Ala Ala Ile Tyr Pro Asn Ser Asp
 210 215 220
 Asp Ile Arg Thr Asp Val Lys Tyr Val His Leu Glu Met Val Gly Glu
 225 230 235 240
 Tyr Gly Ile Ser Val Tyr Thr His Glu Thr Thr His Val Asn Asp Arg
 245 250 255
 Ala Ile Tyr Leu Gly Gly Phe Gly His Arg Glu Gly Thr Asp Ala Glu
 260 265 270
 Ala Tyr Ala Gln Gly Met Leu Gln Thr Pro Val Thr Gly Ser Gly Phe
 275 280 285
 Asp Glu Phe Gly Ser Leu Gly Ile Asn Met Val Phe Lys Arg Lys Asn
 290 295 300
 Asp Gly Asn Gln Trp Tyr Ile Thr Asp Pro Lys Thr Leu Lys Thr Arg
 305 310 315 320
 Glu Asp Ile Asn Arg Tyr Met Lys Gly Tyr Asn Asp Thr Leu Thr Leu
 325 330 335
 Leu Asp Glu Ile Glu Ala Glu Ser Val Ile Ser Gln Gln Asn Lys Asp
 340 345 350
 Leu Asn Ser Ala Trp Phe Lys Lys Ile Asp Arg Glu Tyr Arg Asp Asn
 355 360 365
 Asn Lys Leu Asn Gln Trp Asp Lys Ile Arg Asn Leu Ser Gln Glu Glu
 370 375 380
 Lys Asn Glu Leu Asn Ile Gln Ser Val Asn Asp Leu Val Asp Gln Gln

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385		390		395		400
Leu Met Thr Asn Arg Asn Pro Gly Asn Gly Ile Tyr Lys Pro Glu Ala						
		405		410		415
Ile Ser Tyr Asn Asp Gln Ser Pro Tyr Val Gly Val Arg Met Met Thr						
		420		425		430
Gly Ile Tyr Gly Gly Asn Thr Ser Lys Gly Ala Pro Gly Ala Val Ser						
		435		440		445
Phe Lys His Asn Ala Phe Arg Leu Trp Gly Tyr Tyr Gly Tyr Glu Asn						
		450		455		460
Gly Phe Leu Gly Tyr Ala Ser Asn Lys Tyr Lys Gln Gln Ser Lys Thr						
		465		470		475
Asp Gly Glu Ser Val Leu Ser Asp Glu Tyr Ile Ile Lys Lys Ile Ser						
		485		490		495
Asn Asn Thr Phe Asn Thr Ile Glu Glu Phe Lys Lys Ala Tyr Phe Lys						
		500		505		510
Glu Val Lys Asp Lys Ala Thr Lys Gly Leu Thr Thr Phe Glu Val Asn						
		515		520		525
Gly Ser Ser Val Ser Ser Tyr Asp Asp Leu Leu Thr Leu Phe Lys Glu						
		530		535		540
Ala Val Lys Lys Asp Ala Glu Thr Leu Lys Gln Glu Ala Asn Gly Asn						
		545		550		555
Lys Thr Val Ser Met Asn Asn Thr Val Lys Leu Lys Glu Ala Val Tyr						
		565		570		575
Lys Lys Leu Leu Gln Gln Thr Asn Ser Phe Lys Thr Ser Ile Phe Lys						
		580		585		590

(2) INFORMATION FOR SEQ ID NO: 223:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 460 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 223:

TAAGACAGAT GAACGGAGCA AGGTGTTTGA CTTTTCATT CCCTACTATA CTGCAAAAAA	60
TAAACTCATT GTCAAAAAAT CTGACTTGAC TACTTATCAG TCTGTAAACG ACTTGGCGCA	120
GAAAAAGGTT GGAGCGCAGA AAGGTTTCGAT TCAAGAGACG ATGGCGAAAG ATTTGCTACA	180
AAATTCTTCC CTCGTATCTC TGCCTAAAAA TGGAATTTA ATCACAGATT TAAATCAGG	240
ACAAGTGGAT GCCGTTATCT TTGAAGAACC TGTTTCCAAG GGATTTGTGG AAAATAATCC	300
TGATTTAGCA ATCGCAGACC TCAATTTTGA AAAAGAGCAA GATGATTCCT ACGCGGTAGC	360
CATgAAAAAA GATAGCAAGA AATTGAAGAG GCAGTTCGAT AAAACCATTC AAAAGTTGAA	420

GGAGTCTGGG GAATTAGACA AACTCATTGA GGAAGCCTTA

460

(2) INFORMATION FOR SEQ ID NO:224:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 153 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:224:

Lys Thr Asp Glu Arg Ser Lys Val Phe Asp Phe Ser Ile Pro Tyr Tyr
 1 5 10 15
 Thr Ala Lys Asn Lys Leu Ile Val Lys Lys Ser Asp Leu Thr Thr Tyr
 20 25 30
 Gln Ser Val Asn Asp Leu Ala Gln Lys Lys Val Gly Ala Gln Lys Gly
 35 40 45
 Ser Ile Gln Glu Thr Met Ala Lys Asp Leu Leu Gln Asn Ser Ser Leu
 50 55 60
 Val Ser Leu Pro Lys Asn Gly Asn Leu Ile Thr Asp Leu Lys Ser Gly
 65 70 75 80
 Gln Val Asp Ala Val Ile Phe Glu Glu Pro Val Ser Lys Gly Phe Val
 85 90 95
 Glu Asn Asn Pro Asp Leu Ala Ile Ala Asp Leu Asn Phe Glu Lys Glu
 100 105 110
 Gln Asp Asp Ser Tyr Ala Val Ala Met Lys Lys Asp Ser Lys Lys Leu
 115 120 125
 Lys Arg Gln Phe Asp Lys Thr Ile Gln Lys Leu Lys Glu Ser Gly Glu
 130 135 140
 Leu Asp Lys Leu Ile Glu Glu Ala Leu
 145 150

(2) INFORMATION FOR SEQ ID NO: 225:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 751 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 225:

CTGTGAGAAT CAAGCTACAC CCAAAGAGAC TAGCGCTCAA AAGACAATCG TCCTTGCTAC 60
 AGCTGGCGAC GTGCCACCAT TTGACTACGA AGACAAGGGC AATCTGACAG GCTTTGATAT 120
 CGAAGTTTTA AAGGCAGTAG ATGAAAAACT CAGCGACTAC GAGATTCAAT TCCAAAGAAC 180

CGCCTGGGAG AGCATCTTCC CAGGACTTGA TTCTGGTCAC TATCAGGCTG CGGCCAATAA 240
 CTTGAGTTAC ACAAAGAGC GTGCTGAAAA ATACCTTTAC TCGCTTCCAA TTTCCAACAA 300
 TCCCCTCGTC CTTGTCAGCA ACAAGAAAAA TCCTTTGACT TCTCTTGACC AGATCGCTGG 360
 TAAAACAACA CAAGAGGATA CCGGAACCTC TAACGCTCAA TTCATCAATA ACTGGAATCA 420
 GAAACACACT GATAATCCCG CTACAATTAA TTTTCTGGT GAGGATATTG GTAAACGAAT 480
 CCTAGACCTT GCTAACGGAG AGTTTGATTT CCTAGTTTTT GACAAGGTAT CCGTTCAAAA 540
 GATTATCAAG GACCGTGGTT TAGACCTCTC AGTCGTTGAT TTACCTTCTG CAGATAGCCC 600
 CAGCAATTAT ATCATTTTCT CAAGCGACCA AAAAGAGTTT AAAGAGCAAT TTGATAAAGC 660
 GCTCAAAGAA CTCTATCAAG ACGGAACCCT TGAAAACTC AGCAATACCT ATCTAGGTGG 720
 TTCTTACCTC CCAGATCAAT CTCAGTTACA A 751

(2) INFORMATION FOR SEQ ID NO:226:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 250 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:226:

Cys Glu Asn Gln Ala Thr Pro Lys Glu Thr Ser Ala Gln Lys Thr Ile
 1 5 10 15
 Val Leu Ala Thr Ala Gly Asp Val Pro Pro Phe Asp Tyr Glu Asp Lys
 20 25 30
 Gly Asn Leu Thr Gly Phe Asp Ile Glu Val Leu Lys Ala Val Asp Glu
 35 40 45
 Lys Leu Ser Asp Tyr Glu Ile Gln Phe Gln Arg Thr Ala Trp Glu Ser
 50 55 60
 Ile Phe Pro Gly Leu Asp Ser Gly His Tyr Gln Ala Ala Ala Asn Asn
 65 70 75 80
 Leu Ser Tyr Thr Lys Glu Arg Ala Glu Lys Tyr Leu Tyr Ser Leu Pro
 85 90 95
 Ile Ser Asn Asn Pro Leu Val Leu Val Ser Asn Lys Lys Asn Pro Leu
 100 105 110
 Thr Ser Leu Asp Gln Ile Ala Gly Lys Thr Thr Gln Glu Asp Thr Gly
 115 120 125
 Thr Ser Asn Ala Gln Phe Ile Asn Asn Trp Asn Gln Lys His Thr Asp
 130 135 140
 Asn Pro Ala Thr Ile Asn Phe Ser Gly Glu Asp Ile Gly Lys Arg Ile
 145 150 155 160

00765271-012201

Ser Tyr Leu Pro Asp Gln Ser Gln Leu Gln
245 250

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 33 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

GACTGGATCC TAAAATCTAC GACAATAAAA ATC

33

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 27 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

CTGAGTCGAC TGGTTGTGCT GGTGAG

27

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

GTCAGGATCC AAATTACAAT ACGGACTATG

30

(2) INFORMATION FOR SEQ ID NO: 230:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 28 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 230:

CAGTGTGAC TAACCTAGG TCGGAAAC

28

(2) INFORMATION FOR SEQ ID NO: 231:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 35 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 231:

GACTGGATCC TGAGAATCAA GCTACACCCA AAGAG

35

(2) INFORMATION FOR SEQ ID NO: 232:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 31 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 232:

AGTCAAGCTT TTGTAAGTGA GATTGATCTG G

31

(2) INFORMATION FOR SEQ ID NO: 233:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 37 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 233:

GACTGGATCC TGGTAACCGC TCTTCTCGTA ACGCAGC

37

(2) INFORMATION FOR SEQ ID NO: 234:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 32 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

32

32

(D) TOPOLOGY: linear

45

45

(D) TOPOLOGY: linear

33

33

(D) TOPOLOGY: linear

35

35

(D) TOPOLOGY: linear

32

32

(2) INFORMATION FOR SEQ ID NO: 239:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 38 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 239:

GACTGGATCC TAGCTCAGGT GGAAACGCTG GTTCATCC

38

(2) INFORMATION FOR SEQ ID NO: 240:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 35 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 240:

AGTCAAGCTT ATCAACTTTT CCACCTTCAA CAACC

35

(2) INFORMATION FOR SEQ ID NO: 241:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 37 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 241:

GTCAAGATCT CTCCAATAT GTTAAATCTG CGGATGG

37

(2) INFORMATION FOR SEQ ID NO: 242:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 42 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 242:

AGTCCTGCAG ATCCACATCC GCTTTCATCG GGTAAAGAA GG

42

(2) INFORMATION FOR SEQ ID NO: 243:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 37 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

37

37

40

37

37

(2) INFORMATION FOR SEQ ID NO: 248:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 35 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 248:

AGTCCTGCAG GTTTTTGTTT GCTTGGTATT GGTCG

35

(2) INFORMATION FOR SEQ ID NO: 249:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 41 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 249:

GACTGGATCC TAGTACAAAC TCAAGCACTA GTCAGACAGA G

41

(2) INFORMATION FOR SEQ ID NO: 250:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 34 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 250:

CAGTCTGCAG TTTCAAAGCT TTTTGTATGT CTTC

34

(2) INFORMATION FOR SEQ ID NO: 251:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 37 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 251:

GACTGGATCC TGGCAATTCT GCGGAAGTA AAGATGC

37

(2) INFORMATION FOR SEQ ID NO: 252:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 36 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 252:

AGTCAAGCTT GTTTCATAGC TTTTGTGATT GTTTCG

36

(2) INFORMATION FOR SEQ ID NO: 253:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 40 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 253:

GACTGGATCC TTCACAAGAA AAAACAAAAA ATGAAGATGG

40

(2) INFORMATION FOR SEQ ID NO: 254:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 31 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 254:

AGTCAAGCTT ATCGACGTAG TCTCCGCCTT C

31

(2) INFORMATION FOR SEQ ID NO: 255:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 38 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 255:

GACTGGATCC GAAAGGTCTG TGGTCAAATA ATCTTACC

38

(2) INFORMATION FOR SEQ ID NO: 256:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 37 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 256:

AGTCAAGCTT AGAGTTAACA TGGTGCTTGC CAATAGG

37

(2) INFORMATION FOR SEQ ID NO: 257:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 37 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 257:

GACTGGATCC AAACCTCAGAA AAGAAAGCAG ACAATGC

37

(2) INFORMATION FOR SEQ ID NO: 258:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 36 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 258:

AGTCAAGCTT CCAAACCTGGT TGATCCAAAC CATCTG

36

(2) INFORMATION FOR SEQ ID NO: 259:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 36 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 259:

GACTGGATCC TTCGAAAGGG TCAGAAGGTG CAGACC

36

(2) INFORMATION FOR SEQ ID NO: 260:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 36 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 260:

AGTCAAGCTT CTGTAGGCTT GGTGTGCCCC AGTTGC

36

(2) INFORMATION FOR SEQ ID NO: 261:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 33 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 261:

CTGAGGATCC GGGGATGGCA GCTTTTAAAA ATC

33

(2) INFORMATION FOR SEQ ID NO: 262:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 31 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 262:

CAGTAAGCTT GTTTACCCAT TCACCATTAC C

31

(2) INFORMATION FOR SEQ ID NO: 263:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 263:

CAGTGGATCC AGACGAGCAA AAAATTAAG

29

(2) INFORMATION FOR SEQ ID NO: 264:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 28 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 264:

TCAGAAGCTT GTTTACCCAT TCACCATT

28

(2) INFORMATION FOR SEQ ID NO: 265:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 35 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 265:

GACTGGATCC CTGTGGTGAG GAAGAACTA AAAAG

35

(2) INFORMATION FOR SEQ ID NO: 266:

2025-10-20 14:26:00

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 38 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 266:

CTGAGTCGAC AATATTCTGT AGGAATGCTT CGAATTTG

38

(2) INFORMATION FOR SEQ ID NO: 267:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 38 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 267:

CTGAGGATCC GACTTTTAAC AATAAACTA TTGAAGAG

38

(2) INFORMATION FOR SEQ ID NO: 268:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 33 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 268:

GTCAGTGCAG GTTGTCACCT CCAAAAATCA CGG

33

(2) INFORMATION FOR SEQ ID NO: 269:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 37 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 269:

GACTGGATCC CTTTACAGGT AAACAACTAC AAGTCGG

37

(2) INFORMATION FOR SEQ ID NO: 270:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 32 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

32

32

31

37

32

(2) INFORMATION FOR SEQ ID_NO: 275:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 39 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 275:

ACTGAGATCT TGGTCAAAAG GAAAGTCAGA CAGGAAAGG

39

(2) INFORMATION FOR SEQ ID NO: 276:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 41 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 276:

CAGTAAGCTT ATTCCTGAGC TTTTGTGATA AAGGTTGCGC A

41

(2) INFORMATION FOR SEQ ID NO: 277:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 40 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 277:

ACTGGGATCC GAAGGATAGA TATATTTTAG CATTTGAGAC

40

(2) INFORMATION FOR SEQ ID NO: 278:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 35 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 278:

AGTCAAGCTT CCATGGTATC AAAGGCAAGA CTTGG

35

(2) INFORMATION FOR SEQ ID NO: 279:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 34 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 279:

GTCAGGATCC GGTAGTTAAA GTTGGTATTA ACGG

34

(2) INFORMATION FOR SEQ ID NO: 280:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 36 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 280:

AGTCAAGCTT GCAATTTTTG CGAAGTATTC CAAGAG

36

(2) INFORMATION FOR SEQ ID NO: 281:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 37 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 281:

AGTCGGATCC TTCTTACGAG TTGGGACTGT ATCAAGC

37

(2) INFORMATION FOR SEQ ID NO: 282:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 40 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 282:

AGTCAAGCTT GTTTATTTTT TCCTTACTTA CAGATGAAGG

40

(2) INFORMATION FOR SEQ ID NO: 283:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 37 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 283:

AGTCGGATCC TACTGAGATG CATCATAATC TAGGAGC

37

(2) INFORMATION FOR SEQ ID NO: 284:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 37 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 284:

TCAGCTCGAG TTCTTTGACA TCTCCATCAT AAGTCGC

37

(2) INFORMATION FOR SEQ ID NO: 285:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 35 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 285:

GACTGGATCC GGTTTTGAGA AAGTATTTGC AGGGG

35

(2) INFORMATION FOR SEQ ID NO: 286:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 39 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 286:

CAGTAAGCTT GGATTTTTTC ATGGATGCAA TTTTTTTGG

39

(2) INFORMATION FOR SEQ ID NO: 287:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 43 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 287:

GACTGGATCC GACAACATT ACTATCCATA CAGTAGAGTC AGC

43

(2) INFORMATION FOR SEQ ID NO: 288:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 40 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

40

30

37

36

35

(2) INFORMATION FOR SEQ ID NO: 293:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 34 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 293:

GACTGGATCC TTATAAGGGT GAATTAGAAA AAGG

34

(2) INFORMATION FOR SEQ ID NO: 294:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 33 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 294:

GACTAAGCTT CTTATTAGGA TTGTTAGTAG TTG

33

(2) INFORMATION FOR SEQ ID NO: 295:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 37 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 295:

GACTGGATCC GAATGTTTCAG GCTCAAGAAA GTTCAGG

37

(2) INFORMATION FOR SEQ ID NO: 296:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 36 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 296:

GACTAAGCTT TTCCCCTGAT GGAGCAAAGT AATACC

36

(2) INFORMATION FOR SEQ ID NO: 297:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 40 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 297:

GACTGGATCC CTTGGGTGTA ACCCATATCC AGCTCCTTCC

40

(2) INFORMATION FOR SEQ ID NO: 298:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 34 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 298:

GACTGTCGAC TTCAGCTTGT TTATCTGGGG TTGC

34

(2) INFORMATION FOR SEQ ID NO: 299:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 38 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 299:

GACTGGATCC TAGTGATGGT ACTTGGCAAG GAAAACAG

38

(2) INFORMATION FOR SEQ ID NO: 300:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 35 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 300:

ACTGCTGCAG ATCTTTGCCA CCTAGCTTCT CATTG

35

(2) INFORMATION FOR SEQ ID NO: 301:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 40 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 301:

GTCAGGATCC TGGGATTCAA TATGTCAGAG ATGATACTAG

40

(2) INFORMATION FOR SEQ ID NO: 302:

0076624:04304

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 35 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 302:

CTAGAAGCTT ACGCACCCAT TCACCATTAT CATTG

35

(2) INFORMATION FOR SEQ ID NO: 303:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 35 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 303:

GTCAGGATCC GGATAATAGA GAAGCATTAA AAACC

35

(2) INFORMATION FOR SEQ ID NO: 304:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 36 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 304:

AGTCAAGCTT GACAAAATCT TGAAACTCCT CTGGTC

36

(2) INFORMATION FOR SEQ ID NO: 305:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 35 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 305:

GTCAGGATCC AGATTTTGTC GAGGAGTGTC ATACC

35

(2) INFORMATION FOR SEQ ID NO: 306:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 36 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

AGTCAAGCTT TCCCTTTTTTA CCCTTACGAA TCCAGG

(2) INFORMATION FOR SEQ ID NO: 307:

SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 43 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

GACTGGATCC ATCTGTAGTT TATGCGGATG AAACACTTAT TAC

43

(2) INFORMATION FOR SEQ ID NO: 308:

(A) LENGTH: 34 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

GACTGTCGAC GCTTTGGTAG AGATAGAAGT CATG

34

(2) INFORMATION FOR SEQ ID NO: 309:

SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 38 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

GACTGGATCC TTACTTTGGT ATCGTAGATA CAGCCGGC

38

(2) INFORMATION FOR SEQ ID NO: 310:

(A) LENGTH: 37 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

AGTCAAGCTT TGTTAATTGC GTACCTTCTA AGCGACC

37

(2) INFORMATION FOR SEQ ID NO: 311:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 37 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 311:

GACTGGATCC AGCTAAGGTT GCATGGGATG CGATTTCG

37

(2) INFORMATION FOR SEQ ID NO: 312:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 34 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 312:

GACTGTCGAC CTGGGCTTTA TTAGTTTGAC TAGC

34

(2) INFORMATION FOR SEQ ID NO: 313:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 33 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 313:

CAGTGGATCC CTATCACTAT GTAAATAAAG AGA

33

(2) INFORMATION FOR SEQ ID NO: 314:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 30 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 314:

ACTGAAGCTT TTCTGTCCCT GTTTGAGGCA

30

(2) INFORMATION FOR SEQ ID NO: 315:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 34 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 315:

CAGTGGATCC TGAGACTCCT CAATCAATAA CAAA

34

(2) INFORMATION FOR SEQ ID NO: 316:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 34 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 316:

ACGTAAGCTT ATAATCAGTA GGAGAACTG AACT

34

(2) INFORMATION FOR SEQ ID NO: 317:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 30 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 317:

CAGTGGATCC GGATGCTCAA GAAACTGCGG

30

(2) INFORMATION FOR SEQ ID NO: 318:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 31 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 318:

GACTAAGCTT TTGCCTCTCA TTCTTGCTTC C

31

(2) INFORMATION FOR SEQ ID NO: 319:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 29 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 319:

CAGTGGATCC CGACAAAGGT GAGACTGAG

29

(2) INFORMATION FOR SEQ ID NO: 320:

0076521 04259260

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 320:

36

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 34 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

GACTGGATCC AAATCAATTG GTAGCACAAG ATCC

34

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

CAGTGTCGAC ATTAGGAGCC ACTGGTCTC

29

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 31 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

CAGTGGATCC CAAACAGTCA GCTTCAGGAA C

31

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

30

32

33

30

28

(2) INFORMATION FOR SEQ ID NO: 329:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 32 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 329:

CAGTGGATCC ATGGACAACA GGAAACTGGG AC

32

(2) INFORMATION FOR SEQ ID NO: 330:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 33 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 330:

CAGTAAGCTT ATTAGCTTCT GTACCTGTGT TTG

33

(2) INFORMATION FOR SEQ ID NO: 331:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 41 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 331:

GACTGGATCC CGATGGGCTC AATCCAACCC CAGGTCAAGT C

41

(2) INFORMATION FOR SEQ ID NO: 332:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 40 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 332:

GACTCTGCAG CATAGCTTTA TCCTCTGACA TCATCGTATC

40

(2) INFORMATION FOR SEQ ID NO: 333:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 34 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

097527 04300

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 333:

GACTGGATCC TTCCAATCAA AAACAGGCAG ATGG

34

(2) INFORMATION FOR SEQ ID NO: 334:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 334:

GACTAAGCTT GAGTCCCATA GTCCAAGGCA

30

(2) INFORMATION FOR SEQ ID NO: 335:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 38 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 335:

AGTCGGATCC TATCACAGGA TCGAACGGTA AGACAACC

38

(2) INFORMATION FOR SEQ ID NO: 336:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 34 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 336:

ACTGGTCGAC TTCTTTTAAC TCCGCTACTG TGTC

34

(2) INFORMATION FOR SEQ ID NO: 337:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 38 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 337:

CAGTGGATCC AAGTTCATCG AAGATGGTTG GGAAGTCC

38

(2) INFORMATION FOR SEQ ID NO: 338:

09765974 0133001

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 32 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 338:

GATCGTCGAC CCGCTCCAC ATGCTCAACC TT

32

(2) INFORMATION FOR SEQ ID NO: 339:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 37 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 339:

TGACGGATCC ATCGCTAGCT AGTGAAATGC AAGAAAG

37

(2) INFORMATION FOR SEQ ID NO: 340:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 37 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 340:

TGACAAGCTT ATTCGTTTTT GAACTAGTTG CTTTCGT

37

(2) INFORMATION FOR SEQ ID NO: 341:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 37 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 341:

GACTGGATCC GCACCAGATG GGGCACAAGG TTCAGGG

37

(2) INFORMATION FOR SEQ ID NO: 342:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 35 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

35

(2) INFORMATION FOR SEQ ID NO: 343:

(A) LENGTH: 36 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

36

GACTAGATCT TTTTAACCCA ACTGTTGGTA CTTTCC

(2) INFORMATION FOR SEQ ID NO: 344:

(A) LENGTH: 34 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

34

TGACAAGCTT GTTAGGTGTT ACATTTTGAC CGTC

(2) INFORMATION FOR SEQ ID NO: 345:

(A) LENGTH: 35 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

35

ACTGAGATCT TTTTAACCCA ACTGTTGGTA CTTTC

(2) INFORMATION FOR SEQ ID NO: 346:

(A) LENGTH: 37 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double--
(D) TOPOLOGY: linear

37

GACTAAGCTT TCTACGATAA CGATCATTTT CTTTACC

(2) INFORMATION FOR SEO ID NO: 347:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 38 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 347:

GACTGTGCGAC TCGTAGATAT TTAAGTCTAA GTGAAGCG

38

(2) INFORMATION FOR SEQ ID NO: 348:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 34 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 348:

AGTCAAGCTT GTTAGGTGTT ACATTTTGCA AGTC

34

(2) INFORMATION FOR SEQ ID NO: 349:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 32 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 349:

GACTGGATCC CTTTGGTTTT GAAGGAAGTA AG

32

(2) INFORMATION FOR SEQ ID NO: 350:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 37 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 350:

TGACCTGCAG ACGATTTTTG AAAAATGGAG GTGTATC

37

(2) INFORMATION FOR SEQ ID NO: 351:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 31 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

0076527 042204

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 351:

CAGTGGATCC CTACTACCTC TCGAGAGAAA G

31

(2) INFORMATION FOR SEQ ID NO: 352:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 32 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 352:

ACTGAAGCTT TTCGCTTTTT ACTCGTTTGA CA

32

(2) INFORMATION FOR SEQ ID NO: 353:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 42 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 353:

CAGTGGATCC TAAGGTCAAA AGTCAGACCG CTAAGAAAGT GC

42

(2) INFORMATION FOR SEQ ID NO: 354:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 38 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 354:

CAGTAAGCTT TAGGGTATCC AAATACTGGT TGTTGATG

38

(2) INFORMATION FOR SEQ ID NO: 355:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 36 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 355:

TGACAGATCT TGACGGGTCT CAGGATCAGA CTCAGG

36

(2) INFORMATION FOR SEQ ID NO: 356:

- (A) LENGTH: 36 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 356:

TGACAAGCTT CAAAGACATC CACCTCTTGA CCTTTG

36

(2) INFORMATION FOR SEQ ID NO: 357:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 38 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 357:

GACTGGATCC TAGAGGCTTT GCCAAATGGT GGGGAAGGG

38

(2) INFORMATION FOR SEQ ID NO: 358:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 40 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 358:

GTCAGTCGAC TTGTTGTAAC ACTTTTCGAG GTTTGGTACC

40.

(2) INFORMATION FOR SEQ ID NO: 359:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 33 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 359:

CAGTGGATCC TCAAAAAGAG AAGGAAACT TGG

33

(2) INFORMATION FOR SEQ ID NO: 360:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 34 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 369:

GACTGGATCC GTCCGGCTCT GTCCAGTCCA CTTTTTCAGC G

41

(2) INFORMATION FOR SEQ ID NO: 370:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 33 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 370:

TCAGAAGCTT ATTTTTTGTT TCCTTAATGC GTT

33

(2) INFORMATION FOR SEQ ID NO: 371:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 39 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 371:

GACTGGATCC GGGACAAATT CAAAAAATA GGCAAGAGG

39

(2) INFORMATION FOR SEQ ID NO: 372:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 34 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 372:

GTCAAAGCTT TGGCTCTTTG ATTGCCAACA ACTG

34

(2) INFORMATION FOR SEQ ID NO: 373:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 39 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 373:

GACTGGATCC TCGTACCAG-CAACAAAGCG AGCAAAAGG

39

(2) INFORMATION FOR SEQ ID NO: 374:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 35 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 365:

CTGAGGATCC AATTGTACAA TTAGAAAAAG ATAGC

35

(2) INFORMATION FOR SEQ ID NO: 366:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 34 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 366:

TGACAAGCTT GCGTTGACTA GGTTCTGCAA TGCC

34

(2) INFORMATION FOR SEQ ID NO: 367:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 40 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 367:

GACTGGATCC TCTGACCAAG CAAAAGAAG CAGTCAATGA

40

(2) INFORMATION FOR SEQ ID NO: 368:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 34 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 368:

TCAGCAGCTG ATCATTGACT TTACGATTTG CTCC

34

(2) INFORMATION FOR SEQ ID NO: 369:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 41 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 32 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 374:

GACTAAGCTT ACTTTTTTCT TTTTCCACAC GA

32

(2) INFORMATION FOR SEQ ID NO: 375:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 39 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 375:

CAGTGGATCC GAACCGACAA GTCGCCCACT ATCAAGACT

39

(2) INFORMATION FOR SEQ ID NO: 376:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 33 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 376:

CTGAAAGCTT TGAATTCTCT TTCTTTTCAG GCT

33

(2) INFORMATION FOR SEQ ID NO: 377:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 36 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 377:

TCGAGGATCC GGTTGTCGGC TGGCAATATA TCCCGT

36

(2) INFORMATION FOR SEQ ID NO: 378:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 37 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

34

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38.

(2) INFORMATION FOR SEQ ID NO: 383:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 383:

37

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 34 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

34

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 37 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

37

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 34 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

34

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 41 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 387:

CAGTGGATCC TGGACAGGTG AAAGGTCATG CTACATTGT G

41

(2) INFORMATION FOR SEQ ID NO: 388:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 33 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 388:

GACTAAGCTT CAACCATTGA GACCTTGCAA CAC

33

(2) INFORMATION FOR SEQ ID NO: 389:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 41 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 389:

GTCAGGATCC GATTGCTCCT TTGAAGGATT TGAGAGAAAC C

41

(2) INFORMATION FOR SEQ ID NO: 390:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 41 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 390:

GACTAAGCTT CGATCAAAGA TAAGATAAAT ATATATAAG T

41

(2) INFORMATION FOR SEQ ID NO: 391:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 47 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 391:

GACTGGATCC TAGGTCATAT GGGACTTTTT TTCTACAACA AAATAGG

47

(2) INFORMATION FOR SEQ ID NO: 392:

00765274 012204

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 37 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 392:

TGACAAGCTT ATCTATCAGC TCATTTAATC GTTTTTG

37

(2) INFORMATION FOR SEQ ID NO: 393:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 35 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 393:

CTGAGGATCC CAACGTTGAG AATTATTTGC GAATG

35

(2) INFORMATION FOR SEQ ID NO: 394:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 31 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 394:

TGACAAGCTT GAGTCTACAA AAGTAATGTA C

31

(2) INFORMATION FOR SEQ ID NO: 395:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 35 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 395:

GTCAGGATCC CTACTATCAA TCAAGTTCTT CAGCC

35

(2) INFORMATION FOR SEQ ID NO: 396:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 37 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

00765271 04220

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 396:

TGACAAGCTT GACTGAGGCT TGGACCAGAT TGAAAAG

37

(2) INFORMATION FOR SEQ ID NO: 397:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 36 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 397:

GACTGGATCC GACAAAAACA TTAAACGTC CTGAGG

36

(2) INFORMATION FOR SEQ ID NO: 398:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 34 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 398:

GACTAAGCTT AGCACGAACT GTGACGCTGG TTCC

34

(2) INFORMATION FOR SEQ ID NO: 399:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 35 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 399:

GACTGGATCC TTCTCAGGAG ACCTTTAAAA ATATC

35

(2) INFORMATION FOR SEQ ID NO: 400:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 31 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 400:

GACTAAGCTT GTTGGCCATC TTGTACATAC C

31

(2) INFORMATION FOR SEQ ID NO: 401:

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 401:

31

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 37 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

- AGTCCTGCAG GTATTAGCC CAATAATCTA TAAAGCT

37

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 32 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

- CAGTGGATCC TTACCGCGTT CATCAAGATG TC

32

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 32 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

- GACTAAGCTT GCCAGATGTT GAAAAGAGAG TG

32

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 40 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

GACTGGATCC GTGGATGGGC TTTAACTATC TTCGTATTCG

40

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 33 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

AGTCAAGCTT GCTAGTCTTC ACTTTCCCTT TCC

33

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 34 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

GACTGTCGAC ACTAAACCAG CATCGTTCGC AGGA

3.4

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 35 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

CTGACTGCAG CTTCTTGAAG AAATAATGAT TGTGG

35

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 32 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

'CAGTGGATCC—TGACTACCTT GAAATCCCAC TT

32

(2) INFORMATION FOR SEQ ID NO: 410:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 39 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 410:

CAGTAAGCTT TTTTSTAAGG TTGTAGAATG ATTTCAATC

39

(2) INFORMATION FOR SEQ ID NO: 411:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 35 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 411:

CAGTGTGAC TCGTATCTTT TTTTGGAGCA ATGTT

35

(2) INFORMATION FOR SEQ ID NO: 412:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 33 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 412:

GACTAAGCTT AAATGTTCCG ATACGGGTGA TTG

33

(2) INFORMATION FOR SEQ ID NO: 413:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 33 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 413:

CAGTGGATCC GGACTCTCTC AAAGATGTGA AAG

33

(2) INFORMATION FOR SEQ ID NO: 414:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 34 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 414:

GACTAAGCTT CTTGAGTTTG TCAAGGATTG CTTT

34

(2) INFORMATION FOR SEQ ID NO: 415:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 38 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 415:

CAGTGGATCC CAAGAAATCC TATCATCTCT TCCAGAAG

38

(2) INFORMATION FOR SEQ ID NO: 416:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 33 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 416:

GACTAAGCTT TTCAGAACTA AAAGCCGCAG CTT

33

(2) INFORMATION FOR SEQ ID NO: 417:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 417:

GACTGGATCC ACGAAATGCA GGGCAGACAG

30

(2) INFORMATION FOR SEQ ID NO: 418:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 36 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 418:

CAGTAAGCTT ATCAACATAA TCTAGTAAAT AAGCGT

36

(2) INFORMATION FOR SEQ ID NO: 419:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 36 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 419:

CAGTGGATCC TGTATAGTTT TTAGCGCTTG TTCTTC

36

(2) INFORMATION FOR SEQ ID NO: 420:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 36 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 420:

GTCAAAGCTT TGATAGAGTG TCATAATCTT CTTTAG

36

(2) INFORMATION FOR SEQ ID NO: 421:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 32 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 421:

GACTGGATCC GTGTGTCGAG CATATTCTGA AG

32

(2) INFORMATION FOR SEQ ID NO: 422:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 37 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 422:

CAGTAAGCTT ACTTTTACCA TTTCTTTGTT CTGCATC

37

(2) INFORMATION FOR SEQ ID NO: 423:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 38 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 423:

GACTGTCGAC GTGTTTGGAT AGCATTCAGA ATCAGACG

38

(2) INFORMATION FOR SEQ ID NO: 424:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 32 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 424:

CAGTAAGCTT CGGAAGTAAA GACAATTTTT CC

32

(2) INFORMATION FOR SEQ ID NO: 425:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 37 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 425:

CAGTGGATCC GTGCCTAGAT AGTATTATTA CTCAAAC

37

(2) INFORMATION FOR SEQ ID NO: 426:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 34 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 426:

GACTAAGCTT TTTGCTTATT TCTCTCAATT TTTC

34

(2) INFORMATION FOR SEQ ID NO: 427:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 36 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 427:

CAGTGGATCC CATTGAGAAG CAGACCTATC AAAATC

36

(2) INFORMATION FOR SEQ ID NO: 428:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 43 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 428:

ACTGAAGCTT ATGTAATTTT TTAGATTTTT CAATATTTTT CAG

43

(2) INFORMATION FOR SEQ ID NO: 429:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 35 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 429:

AGTCGGATCC TAAGGCTGAT AATCGTGTTT AAATG

35

(2) INFORMATION FOR SEQ ID NO: 430:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 31 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 430:

GACTAAGCTT AAAATTAGAT AGACGTTGAG T

31

(2) INFORMATION FOR SEQ ID NO: 431:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 35 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 431:

AGTCGGATCC CTGTGGCAAT CAGTCAGCTG CTTCC

35

(2) INFORMATION FOR SEQ ID NO: 432:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 40 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 432:

GACTGTCGAC TTTAATCTTG TCCCAGGTGG TTAATTTGCC

40

(2) INFORMATION FOR SEQ ID NO: 433:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 38 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 433:

ACTGGTCGAC TTGTCAACAA CAACATGCTA CTTCTGAG

38

(2) INFORMATION FOR SEQ ID NO: 434:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 35 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 434:

GACTCTGCAG AAGTTTAACC CACTTATCAT TATCC

35

(2) INFORMATION FOR SEQ ID NO: 435:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 39 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 435:

ACTGGGATCC TTGTTCAAGC AAGTCCGTGA CTAGTGAAC

39

(2) INFORMATION FOR SEQ ID NO: 436:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 33 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 436:

GACTAAGCTT GGCTAATTCC TTCAAAGTTT GCA

33

(2) INFORMATION FOR SEQ ID NO: 437:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 39 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 437:

AGTCGGATCC CTCGCAAATT GAAAAGGCGG CAGTTAGCC

39

(2) INFORMATION FOR SEQ ID NO: 438:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 35 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 438:

GACTAAGCTT GTAAATAAGC GTACCTTTTT CTTCC

35

(2) INFORMATION FOR SEQ ID NO: 439:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 38 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 439:

TCAGGGATCC TTGTCAGTCA GGTCTAATG GTTCTCAG

38

(2) INFORMATION FOR SEQ ID NO: 440:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 32 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 440:

AGTCAAGCTT GGCATTGGCG TCGCCGTCCT TC

32

(2) INFORMATION FOR SEQ ID NO: 441:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 38 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

38

34

37

31

39

(2) INFORMATION FOR SEQ ID NO: 446:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 37 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 446:

GACTGTCGAC TACTTGACCG AATGCGTCGA ATGTACG

37

(2) INFORMATION FOR SEQ ID NO: 447:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 34 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 447:

CTGAGGATCC ATTAGACAGA TTAATTGAAA TCGG

34

(2) INFORMATION FOR SEQ ID NO: 448:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 34 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 448:

GACTGTCGAC TTAAAGATT GAAGTTTAA AGCT

34

(2) INFORMATION FOR SEQ ID NO: 449:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 35 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 449:

TGACGGATCC TAAGACAGAT GAACGGAGCA AGGTG

35

(2) INFORMATION FOR SEQ ID NO: 450:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 35 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

35

33

34

CTGAAAGCTT TTGTAAGTGA GATTGATCTG GGAG